



FIGURE 10

Figure 10. Oligonucleotide Primers for QuikChange Mutagenesis

V93E#1

5'-gAACATCCCCAAGATgAACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 5)

V93E#2

5'-CTTTTCTCTAATAgTgggTTCATCTTggggATgTTC-3' (SEQ ID NO: 6)

V93R#1

5'-gAACATCCCCAAGATAgACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 7)

V93R#2

5'-CTTTTCTCTAATAgTgggTCTATCTTggggATgTTC-3' (SEQ ID NO: 8)

V93N#1

5'-gAACATCCCCAAGATAACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 9)

V93N#2

5'-CTTTTCTCTAATAgTggggTTATCTTggggATgTTC-3' (SEQ ID NO: 10)

V93H#1

5'-gAACATCCCCAAGATCACCACTATTAgAgAAAAAg-3' (SEQ ID NO: 11)

V93H#2

5'-CTTTTCTCTAATAgTggggTgATCTTggggATgTTC-3' (SEQ ID NO: 12)

V93X (for saturation mutagenesis; obtained V93G and V93L mutants from library)

5'-(Phosphate)gAACATCCCCAAGATNNKCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 13)

V93K#1

5'-gAACATCCCCAAGATAACCCACTATTAgAg-3' (SEQ ID NO: 14)

V93K#2

5'-CTCTAATAgTgggTTTATCTTggggATgTTC-3' (SEQ ID NO: 15)

QCM#1 5'-(Phosphate)gAACATCCCCAAGATgCCCCACTATTAgAgAAAAAg-(SEQ ID NO: 16)'

Alanine

QCM#2 5'-(Phosphate)gAACATCCCCAAGATgACCCCACTATTAgAgAAAAAg-3'(SEQ ID NO: 17)

Aspartic Acid

QCM#3 5'-(Phosphate)gAACATCCCCAAGATTgCCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 18)

Cysteine

QCM#4 5'-(Phosphate)gAACATCCCCAAGATATACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 19)

Isoleucine

QCM#5 5'-(Phosphate)gAACATCCCCAAGATATgCCCACCTATTAgAgAAAAAg-3' (SEQ ID NO: 20)

Methionine

QCM#6 5'-(Phosphate)gAACATCCCCAAGATTTCCCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 21)

Replacement Figure

Phenylalanine

QCM#7 5'-(Phosphate)gAACATCCCCAAGATCCTCCCCTATTAgAgAAAAAg-3' (SEQ ID NO: 22)

Proline

QCM#8 5'-(Phosphate)gAACATCCCCAAGATAgCCCCCTATTAgAgAAAAAg-3' (SEQ ID NO: 23)

Serine

QCM#9 5'-(Phosphate)gAACATCCCCAAGATACCCCCTATTAgAgAAAAAg- 3' (SEQ ID NO: 24)

Threonine

QCM#10 5'-(Phosphate)gAACATCCCCAAGATTACCCCCTATTAgAgAAAAAg-3' (SEQ ID NO: 25)

Tyrosine

QCM#11 5'-(Phosphate)gAACATCCCCAAGATTggCCCCTATTAgAgAAAAAg-3'

(SEQ ID NO: 26)

Tryptophan

FIGURE 13A

PFU DNA POLYMERASE

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 27)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 28)

```
ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAAGCTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTGCGACTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTA AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTC AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAATA AATCCTAG 2328
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PFU DNA POLYMERASE

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 29)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 30)

```
ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAGTGCCCTG GGGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGCCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
```

PFU DNA POLYMERASE

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 31)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 32)

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ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
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CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTGACTTGT 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGGTGGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAAGAAA 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

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KOD DNA POLYMERASE

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 33)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 34)

```

ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTAAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACNNNC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACCTTGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GGCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780

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TATCCTGTGA	TAAGACGGAC	GATAAACCTG	CCCACATACA	CGCTTGAGGC	CGTTTATGAA	840
GCCGTCTTCG	GTCAGCCGAA	GGAGAAGGTT	TACGCTGAGG	AAATAACCAC	AGCCTGGGAA	900
ACCGGCGAGA	ACCTTGAGAG	AGTCGCCCCG	TACTCGATGG	AAGATGCGAA	GGTCACATAC	960
GAGCTTGGGA	AGGAGTTCCT	TCCGATGGAG	GCCCAGCTTT	CTCGCTTAAT	CGGCCAGTCC	1020
CTCTGGGACG	TCTCCCGCTC	CAGCACTGGC	AACCTCGTTG	AGTGGTTCCT	CCTCAGGAAG	1080
GCCTATGAGA	GGAATGAGCT	GGCCCCGAAC	AAGCCCCGATG	AAAAGGAGCT	GGCCAGAAGA	1140
CGGCAGAGCT	ATGAAGGAGG	CTATGTAAAA	GAGCCCCGAGA	GAGGGTTGTG	GGAGAACATA	1200
GTGTACCTAG	ATTTTAGATC	CCTGTACCCC	TCAATCATCA	TCACCCACAA	CGTCTCGCCG	1260
GATACGCTCA	ACAGAGAAGG	ATGCAAGGAA	TATGACGTTG	CCCCACAGGT	CGGCCACCGC	1320
TTCTGCAAGG	ACTTCCCAGG	ATTTATCCCC	AGCCTGCTTG	GAGACCTCCT	AGAGGAGAGG	1380
CAGAAGATAA	AGAAGAAGAT	GAAGGCCACG	ATTGACCCGA	TCGAGAGGAA	GCTCCTCGAT	1440
TACAGGCAGA	GGGCCATCAA	GATCCTGGCA	AACAGCTACT	ACGGTTACTA	CGGCTATGCA	1500
AGGGCGCGCT	GGTACTGCAA	GGAGTGTGCA	GAGAGCGTAA	CGGCCTGGGG	AAGGGAGTAC	1560
ATAACGATGA	CCATCAAGGA	GATAGAGGAA	AAGTACGGCT	TTAAGGTAAT	CTACAGCGAC	1620
ACCGACGGAT	TTTTTGCCAC	AATACCTGGA	GCCGATGCTG	AAACCGTCAA	AAAGAAGGCT	1680
ATGGAGTTCC	TCAAGTATAT	CAACGCCAAA	CTTCCGGGCG	CGCTTGAGCT	CGAGTACGAG	1740
GGCTTCTACA	AACGCGGCTT	CTTCGTCACG	AAGAAGAAGT	ATGCGGTGAT	AGACGAGGAA	1800
GGCAAGATAA	CAACGCGCGG	ACTTGAGATT	GTGAGGCGTG	ACTGGAGCGA	GATAGCGAAA	1860
GAGACGCAGG	CGAGGGTTCT	TGAAGCTTTG	CTAAAGGACG	GTGACGTCGA	GAAGGCCGTG	1920
AGGATAGTCA	AAGAAGTTAC	CGAAAAGCTG	AGCAAGTACG	AGGTTCCGCC	GGAGAAGCTG	1980
GTGATCCACG	AGCAGATAAC	GAGGGATTTA	AAGGACTACA	AGGCAACCGG	TCCCCACGTT	2040
GCCGTTGCCA	AGAGGTTGGC	CGCGAGAGGA	GTCAAAATAC	GCCCTGGAAC	GGTGATAAGC	2100
TACATCGTGC	TCAAGGGCTC	TGGGAGGATA	GGCGACAGGG	CGATACCGTT	CGACGAGTTC	2160
GACCCGACGA	AGCACAAGTA	CGACGCCGAG	TACTACATTG	AGAACCAGGT	TCTCCGAGCC	2220
GTTGAGAGAA	TTCTGAGAGC	CTTCGGTTAC	CGCAAGGAAG	ACCTGCGCTA	CCAGAAGACG	2280
AGACAGGTTG	GTTTGAGTGC	TTGGCTGAAG	CCGAAGGGAA	CTTGA	2325	

Vent DNA POLYMERASE

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 35)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 36)

ATGATACTGG	ACACTGATTA	CATAACAAAA	GATGGCAAGC	CTATAATCCG	AATTTTTTAAG	60
AAAGAGAACG	GGGAGTTTAA	AATAGAACTT	GACCCTCATT	TTCAGCCCTA	TATATATGCT	120
CTTCTCAAAG	ATGACTCCGC	TATTGAGGAG	ATAAAGGCAA	TAAAGGGCGA	GAGACATGGA	180
AAAAGTGTGA	GAGTGCTCGA	TGCAGTGAAG	GTCAGGAAAA	AATTTTTTGGG	AAGGGAAGTT	240
GAAAGTCTGGA	AGCTCATTTT	CGAGCATCCC	CAAGACNNNC	CAGCTATGCG	GGGCAAAATA	300
AGGGAACATC	CAGCTGTGGT	TGACATTTAC	GAATATGACA	TACCCCTTGC	CAAGCGTTAT	360
CTCATAGACA	AGGGCTTGAT	TCCCATGGAG	GGAGACGAGG	AGCTTAAGCT	CCTTGCCTTT	420
GATATTGAAA	CGTTTTATCA	TGAGGGAGAT	GAATTTGGAA	AGGGCGAGAT	AATAATGATT	480
AGTTATGCCG	ATGAAGAAGA	GGCCAGAGTA	ATCACATGGA	AAAAATATCGA	TTTGCCGTAT	540
GTCGATGTTG	TGTCCAATGA	AAGAGAAAATG	ATAAAGCGTT	TTGTTCAAGT	TGTTAAAGAA	600
AAAGACCCCG	ATGTGATAAT	AACTTACAAT	GGGGACAATT	TTGATTTTGC	GTATCTCATA	660
AAACGGGCGG	AAAAGCTGGG	AGTTCGGCTT	GTCTTAGGAA	GGGACAAAGA	ACATCCCGAA	720
CCCAAGATTG	AGAGGATGGG	TGATAGTTTT	GCTGTGGAAA	TCAAGGGTAG	AATCCACTTT	780
GATCTTTTCC	CAGTTGTGCG	AAGGACGATA	AACCTCCCAA	CGTATACGCT	TGAGGCAGTT	840
TATGAAGCAG	TTTTAGGAAA	AACCAAAAGC	AAATTAGGAG	CAGAGGAAAT	TGCCGCTATA	900
TGGGAAACAG	AAGAAAGCAT	GAAAAAACTA	GCCCAGTACT	CAATGGAAGA	TGCTAGGGCA	960
ACGTATGAGC	TCGGGAAGGA	ATTCTTCCCC	ATGGAAGCTG	AGCTGGCAAA	GCTGATAGGT	1020
CAAAGTGTAT	GGGACGTCTC	GAGATCAAGC	ACCGGCAACC	TCGTGGAGTG	GTATCTTTTA	1080
AGGGTGGCAT	ACGCGAGGAA	TGAAC TTGCA	CCGAACAAAC	CTGATGAGGA	AGAGTATAAA	1140
CGGCGCTTAA	GAACAACTTA	CCTGGGAGGA	TATGTAAAAG	AGCCAGAAAA	AGGTTTGTGG	1200
GAAAATATCA	TTTATTTTGA	TTTCCGCAGT	CTGTACCCTT	CAATAATAGT	TACTCACAAC	1260
GTATCCCCAG	ATACCCTTGA	AAAAGAGGGC	TGTAAGAATT	ACGATGTTGC	TCCGATAGTA	1320
GGATATAGGT	TCTGCAAGGA	CTTTCCGGGC	TTTATTCCTT	CCATACTCGG	GGACTTAATT	1380
GCAATGAGGC	AAGATATAAA	GAAGAAAATG	AAATCCACAA	TTGACCCGAT	CGAAAAGAAA	1440
ATGCTCGATT	ATAGGCAAAG	GGCTATTAAA	TTGCTTGCAA	ACAGCTATTA	CGGCTATATG	1500

GGGTATCCTA	AGGCAAGATG	GTACTCGAAG	GAATGTGCTG	AAAGCGTTAC	CGCATGGGGG	1560
AGACACTACA	TAGAGATGAC	GATAAGAGAA	ATAGAGGAAA	AGTTCGGCTT	TAAGGTTCTT	1620
TATGCGGACA	CTGACGGCTT	TTATGCCACA	ATACCCGGGG	AAAAGCCTGA	ACTCATTA	1680
AAGAAAGCCA	AGGAATTCCT	AAACTACATA	AACTCCAAAC	TTCCAGGTCT	GCTTGAGCTT	1740
GAGTATGAGG	GCTTTTACTT	GAGAGGATTC	TTTGTTACAA	AAAAGCGCTA	TGCAGTCATA	1800
GATGAAGAGG	GCAGGATAAC	AACAAGGGGC	TTGGAAGTAG	TAAGGAGAGA	TTGGAGTGAG	1860
ATAGCTAAGG	AGACTCAGGC	AAAGGTTTTA	GAGGCTATAC	TTAAAGAGGG	AAGTGTGAA	1920
AAAGCTGTAG	AAGTTGTTAG	AGATGTTGTA	GAGAAAAATAG	CAAAATACAG	GGTTCACCTT	1980
GAAAAGCTTG	TTATCCATGA	GCAGATTACC	AGGGATTTAA	AGGACTACAA	AGCCATTGGC	2040
CCTCATGTGC	CGATAGCAAA	AAGACTTGCC	GCAAGAGGGA	TAAAAGTGAA	ACCGGGCACA	2100
ATAATAAGCT	ATATCGTTCT	CAAAGGGAGC	GGAAAGATAA	GCGATAGGGT	AATTTTACTT	2160
ACAGAATACG	ATCCTAGAAA	ACACAAGTAC	GATCCGGACT	ACTACATAGA	AAACCAAGTT	2220
TTGCCGGCAG	TACTTAGGAT	ACTCGAAGCG	TTTGATACAA	GAAAGGAGGA	TTTAAGGTAT	2280
CAAAGCTCAA	AACAAACCGG	CTTAGATGCA	TGGCTCAAGA	GGTAG	2325	

Deep Vent

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 37)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 38)

ATGATACTTG	ACGCTGACTA	CATCACCGAG	GATGGGAAGC	CGATTATAAG	GATTTTCAAG	60
AAAGAAAACG	GCGAGTTTAA	GGTTGAGTAC	GACAGAAACT	TTAGACCTTA	CATTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAA	GTAAGGAAGA	AGTTCTTGGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCCT	CAGGACNNNC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTCCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGGCCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAAAG	GACTGGAGAG	AGTTGCAAAG	TATTCATGGA	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCA	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACGGAG	GAAAAGTTTC	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCCT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTTCGT	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTGCATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220

GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAGTAA 2328

JDF-3

V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 39)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 40)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCCTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCA
GGATTGAATACGACCGCGAGTTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAA
GATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAAGTTCTCGGCAGGTCT
GTGGAGGTCTGGGTCTCTACTTCACGCACCCGACGACNNNCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGG
TCATCGACATCTACGAGTACGACATACCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGA
GGAAGAGCTTAAACTCATGTCTTTCGACATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGGAAACGGGGCCGATTCTG
ATGATAAGCTACGCCGATGAAAGCGAGGCGCGCTGATAACCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCT
CCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATAACCGG
CGACAACCTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTACCTCGGGAGGGACGGGAGC
GAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCA
TAAGGCGCACCATAAACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGT
CTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGGACCGG
AGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGG
ACGTTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCTCCTAAGGAAGGCCTACGAGAGGAACGAACTCGCTCC
CAACAAGCCCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGCTACGCGCGGTGGCTACGTCAAGGAGCCGGAGCGGGGA
CTGTGGGACAATATCGTGTATCTAGACTTTTCGTAGTCTCTACCTTCAATCATAATCACCCACAACGTCTCGCCAGATA
CGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCGAGGTCCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTT
CATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTG
GAGAAGAATCTCCTCGATTACAGGCAACGCCTCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCA
GGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGA
GCTTGAGGAAAAGTTCCGTTTTAAAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCT
GAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAACTATATCAATCCCAAAGTCCCGGCCTTCTCGAACTCGAATACG
AGGGCTTCTACGTACGGGGCTTCTTCGTACGAAGAAAAAGTACGCGGTTCATCGACGAGGAGGGCAAGATAACCACGCG
CGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGCGAGGCGAGGGTTTTGGAGGCGATACTCAGG
CACGGTGACGTTGAAGAGGCCGTCAGAATTGTCAGGGAAAGTCACCGAAAAAGCTGAGCAAGTACGAGGTTCCGCCCGGAGA
AGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAgCG
TTTGGCCGCCAGAGGTGTTAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGC
GACAGGGCGATTCCCTTCGACGAGTTGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTTC
TGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGG
GCTTGGCGCGTGGCTGAAGCCGAAGGGGAAGAAGAAGTGA

Figure 13B

>Pfu V93R (SEQ ID NO:41)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDL PYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLD FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS //

>Pfu V93E (SEQ ID NO:42)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDL PYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLD FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/G387P (SEQ ID NO:43)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDL PYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TPGFVKEPEKGLWENIVYLD FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/D141A/E143A (SEQ ID NO:44)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDL PYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIFHDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLD FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

Replacement Figure

>Pfu V93E/G387P (SEQ ID NO:45)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEEMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TPGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEEDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKK

>Pfu V93E/D141A/E143A (SEQ ID NO:46)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVVSSEEMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEEDPKKHKYDAEYYIENQVLPVAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKK

>DEEP VENT V93R (SEQ ID NO:47)

MILDADYITEDGKPIIRIFKKENGKFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDRPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEEAKVITWKKIDLPHYVEVVSSEEMIKRFLKVIREKDPDVIITYNGDSFDFPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSTGNLVEWYLLRKAYERNELAPNKPDEREYERRRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLKRLDERQ
EIKRKMASKDPIEKMLDYRQRAIKILANSYGYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEDLRKHKYDAEYYIENQVLPVAVLRILEAFGYRKEDLRWQTKQTGLTAWL
NIKKK

>DEEP VENT V93E (SEQ ID NO:48)

MILDADYITEDGKPIIRIFKKENGKFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDEPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEEAKVITWKKIDLPHYVEVVSSEEMIKRFLKVIREKDPDVIITYNGDSFDFPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSTGNLVEWYLLRKAYERNELAPNKPDEREYERRRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLKRLDERQ
EIKRKMASKDPIEKMLDYRQRAIKILANSYGYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEDLRKHKYDAEYYIENQVLPVAVLRILEAFGYRKEDLRWQTKQTGLTAWL
NIKKK

>TGO V93R (SEQ ID NO:49)

Replacement Figure

MILDTDYITEDGKPVIRIFKKENGFEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTRVRVRAEKVKKKFLG
RPIEVWKLYFTHPQDRPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPHYVDVSTEEKEMIKRFLKVVEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIFHDLYPVIRRTINLPTYTLEAVYEAFI GQPKVKVYAEIEAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFKCKDFPGFIPSLLDLLEERQK
VKKMKATIDPIEKLLDYRQRAIKILANSFYGGYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIEYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>TGO V93E (SEQ ID NO:50)

MILDTDYITEDGKPVIRIFKKENGFEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTRVRVRAEKVKKKFLG
RPIEVWKLYFTHPQDEPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPHYVDVSTEEKEMIKRFLKVVEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIFHDLYPVIRRTINLPTYTLEAVYEAFI GQPKVKVYAEIEAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFKCKDFPGFIPSLLDLLEERQK
VKKMKATIDPIEKLLDYRQRAIKILANSFYGGYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIEYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>KOD V93R (SEQ ID NO:51)

MILDTDYITEDGKPVIRIFKKENGFEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDRPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLTYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPHYVDVSTEREMIKRFLRVVVEKDPDVLITYNGDNFDFAYLKKRCEKLGINF
LGRDGSEPKIQRMGDRFAVEVKGRIFHDLYPVIRRTINLPTYTLEAVYEA VFGQPKVKVYAEIEIPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYGGYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFVKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKGDVKEAVRIVKEVTEKLSKYEVPPEKLVIEHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>KOD V93E (SEQ ID NO:52)

MILDTDYITEDGKPVIRIFKKENGFEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDEPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLTYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPHYVDVSTEREMIKRFLRVVVEKDPDVLITYNGDNFDFAYLKKRCEKLGINF
LGRDGSEPKIQRMGDRFAVEVKGRIFHDLYPVIRRTINLPTYTLEAVYEA VFGQPKVKVYAEIEIPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYGGYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFVKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKGDVKEAVRIVKEVTEKLSKYEVPPEKLVIEHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>VENT V93R (SEQ ID NO:53)

MILDTDYITKDGKPIIRIFKKENGFEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHKGKTVRVLDVAVKVRKKFLG
REVEVWKLIFEHPQDRPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDLPHYVDVVSNEREMIKRFVQVVEKDPDVIITYNGDNFDPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRTINLPTYTLEAVYEAVLGKTKSKLGAEIEAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAEALAKLIGQSVWDVSRSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSIILGDLIAM
RQDIKKMKSTIDPIEKKMLDYLQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGIFYATIPGEKPELIKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIEHQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYIENQVLPVAVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>VENT V93E (SEQ ID NO:54)

MILDTDYITKDGKPIIRIFKKENGFEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHKGKTVRVLDVAVKVRKKFLG
REVEVWKLIFEHPQDEPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDLPHYVDVVSNEREMIKRFVQVVEKDPDVIITYNGDNFDPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRTINLPTYTLEAVYEAVLGKTKSKLGAEIEAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAEALAKLIGQSVWDVSRSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSIILGDLIAM
RQDIKKMKSTIDPIEKKMLDYLQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGIFYATIPGEKPELIKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIEHQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYIENQVLPVAVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>JDF-3 V93R (SEQ ID NO:55)

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDSIAIEEIKKITAERHGRVVKVRAEKVKKKFLGR
SVEVWVLYFTHPQDRPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSPDITLYHEGEEFGTGP
ILMISYADESEARVITWKKIDLPHYVEVVSTEEKEMIKRFLRVVEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPKIQRMGDRFAVEVKGRVHFDLPHYVIRRTINLPTYTLEAVYEAVFGKPKVKYAEIATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGYAGGYVK
EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFKDFPGFIPSLGNLLEERQKIKRKM
ATLDPLEKNLLDYRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYIENQVLPVAVRILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

>JDF-3 V93E (SEQ ID NO:56)

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDSIAIEEIKKITAERHGRVVKVRAEKVKKKFLGR
SVEVWVLYFTHPQDEPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSPDITLYHEGEEFGTGP
ILMISYADESEARVITWKKIDLPHYVEVVSTEEKEMIKRFLRVVEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPKIQRMGDRFAVEVKGRVHFDLPHYVIRRTINLPTYTLEAVYEAVFGKPKVKYAEIATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGYAGGYVK
EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFKDFPGFIPSLGNLLEERQKIKRKM
ATLDPLEKNLLDYRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYIENQVLPVAVRILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

Replacement Figure

Figure 14

Tgo 93:

NNN = AGA, AGG, CGA, CGC, CGG, CGT (R)

(NUCLEOTIDE SEQUENCE: SEQ ID NO: 57; AMINO ACID SEQUENCE: SEQ ID NO: 58)

NNN = GAA, GAG (E)

(NUCLEOTIDE SEQUENCE: SEQ ID NO: 59; AMINO ACID SEQUENCE: SEQ ID NO: 60)

5'

atg atc ctc gat aca gac tac ata act gag gat gga aag ccc gtc atc	48
Met Ile Leu Asp Thr Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile	
1 5 10 15	
agg atc ttc aag aag gag aac ggc gag ttc aaa ata gac tac gac aga	96
Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Asp Tyr Asp Arg	
20 25 30	
aac ttt gag cca tac atc tac gcg ctc ttg aag gac gac tct gcg att	144
Asn Phe Glu Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile	
35 40 45	
gag gac gtc aag aag ata act gcc gag agg cac ggc act acc gtt agg	192
Glu Asp Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Thr Val Arg	
50 55 60	
gtt gtc agg gcc gag aaa gtg aag aag aag ttc cta ggc agg ccg ata	240
Val Val Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Pro Ile	
65 70 75 80	
gag gtc tgg aag ctc tac ttc act cac ccc cag gac nnn ccc gca atc	288
Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Xaa Pro Ala Ile	
85 90 95	
agg gac aag ata aag gag cat cct gcc gtt gtg gac atc tac gag tac	336
Arg Asp Lys Ile Lys Glu His Pro Ala Val Val Asp Ile Tyr Glu Tyr	
100 105 110	
gac atc ccc ttc gcg aag cgc tac ctc ata gac aaa ggc tta atc ccg	384
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro	
115 120 125	
atg gag ggc gac gag gaa ctt aag atg ctc gcc ttc gac atc gag acg	432
Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr	
130 135 140	
ctc tat cac gag ggc gag gag ttc gcc gaa ggg cct atc ctg atg ata	480
Leu Tyr His Glu Gly Glu Glu Phe Ala Glu Gly Pro Ile Leu Met Ile	
145 150 155 160	
agc tac gcc gac gag gaa ggg gcg cgc gtt att acc tgg aag aat atc	528
Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Ile	
165 170 175	
gac ctt ccc tat gtc gac gtc gtt tcc acc gag aag gag atg ata aag	576
Asp Leu Pro Tyr Val Asp Val Val Ser Thr Glu Lys Glu Met Ile Lys	
180 185 190	

Replacement Figure

cgc ttc ctc aag gtc gtc aag gaa aag gat ccc gac gtc ctc ata acc	624
Arg Phe Leu Lys Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr	
195 200 205	
tac aac ggc gac aac ttc gac ttc gcc tac ctc aag aag cgc tcc gag	672
Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Ser Glu	
210 215 220	
aag ctc gga gtc aag ttc atc ctc gga agg gaa ggg agc gag ccg aaa	720
Lys Leu Gly Val Lys Phe Ile Leu Gly Arg Glu Gly Ser Glu Pro Lys	
225 230 235 240	
atc cag cgc atg ggc gat cgc ttt gcg gtg gag gtc aag gga agg att	768
Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Ile	
245 250 255	
cac ttc gac ctc tac ccc gtc att agg aga acg att aac ctc ccc act	816
His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr	
260 265 270	
tac acc ctt gag gca gta tat gaa gcc atc ttt gga cag ccg aag gag	864
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Gln Pro Lys Glu	
275 280 285	
aag gtc tac gct gag gag ata gcg cag gcc tgg gaa acg ggc gag gga	912
Lys Val Tyr Ala Glu Glu Ile Ala Gln Ala Trp Glu Thr Gly Glu Gly	
290 295 300	
tta gaa agg gtg gcc cgc tac tcg atg gag gac gca aag gta acc tat	960
Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr	
305 310 315 320	
gaa ctc gga aaa gag ttc ttc cct atg gaa gcc cag ctc tcg cgc ctc	1008
Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu	
325 330 335	
gta ggc cag agc ctc tgg gat gta tct cgc tcg agt acc gga aac ctc	1056
Val Gly Gln Ser Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu	
340 345 350	
gtc gag tgg ttt ttg ctg agg aag gcc tac gag agg aat gaa ctt gca	1104
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala	
355 360 365	
cca aac aag ccg gac gag agg gag ctg gca aga aga agg gag agc tac	1152
Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Glu Ser Tyr	
370 375 380	
gcg ggt gga tac gtc aag gag ccc gaa agg gga ctg tgg gag aac atc	1200
Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile	
385 390 395 400	
gtg tat ctg gac ttc cgc tcc ctg tat cct tcg ata ata atc acc cat	1248
Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His	
405 410 415	
aac gtc tcc cct gat aca ctc aac agg gag ggt tgt gag gag tac gac	1296

Replacement Figure

Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Glu	Glu	Tyr	Asp		
			420					425					430				
gtg	gct	cct	cag	gta	ggc	cat	aag	ttc	tgc	aag	gac	ttc	ccc	ggc	ttc	1344	
Val	Ala	Pro	Gln	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Phe	Pro	Gly	Phe		
			435				440					445					
atc	cca	agc	ctc	ctc	gga	gac	ctc	ttg	gag	gag	aga	cag	aag	gta	aag	1392	
Ile	Pro	Ser	Leu	Leu	Gly	Asp	Leu	Leu	Glu	Glu	Arg	Gln	Lys	Val	Lys		
	450					455					460						
aag	aag	atg	aag	gcc	act	ata	gac	cca	atc	gag	aag	aaa	ctc	ctc	gat	1440	
Lys	Lys	Met	Lys	Ala	Thr	Ile	Asp	Pro	Ile	Glu	Lys	Lys	Leu	Leu	Asp		
465					470					475					480		
tac	agg	caa	cga	gca	atc	aaa	atc	ctt	gct	aat	agc	ttc	tac	ggc	tac	1488	
Tyr	Arg	Gln	Arg	Ala	Ile	Lys	Ile	Leu	Ala	Asn	Ser	Phe	Tyr	Gly	Tyr		
				485				490						495			
tac	ggc	tat	gca	aag	gcc	cgc	tgg	tac	tgc	aag	gag	tgc	gcc	gag	agc	1536	
Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	Ser		
			500					505					510				
gtt	acc	gct	tgg	ggc	agg	cag	tac	atc	gag	acc	acg	ata	agg	gaa	ata	1584	
Val	Thr	Ala	Trp	Gly	Arg	Gln	Tyr	Ile	Glu	Thr	Thr	Ile	Arg	Glu	Ile		
		515					520					525					
gag	gag	aaa	ttt	ggc	ttt	aaa	gtc	ctc	tac	gcg	gac	aca	gat	gga	ttt	1632	
Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ala	Asp	Thr	Asp	Gly	Phe		
	530					535					540						
ttc	gca	aca	ata	cct	gga	gcg	gac	gcc	gaa	acc	gtc	aaa	aag	aag	gca	1680	
Phe	Ala	Thr	Ile	Pro	Gly	Ala	Asp	Ala	Glu	Thr	Val	Lys	Lys	Lys	Ala		
545					550				555						560		
aag	gag	ttc	ctg	gac	tac	atc	aac	gcc	aaa	ctg	ccc	ggc	ctg	ctc	gaa	1728	
Lys	Glu	Phe	Leu	Asp	Tyr	Ile	Asn	Ala	Lys	Leu	Pro	Gly	Leu	Leu	Glu		
				565				570					575				
ctc	gaa	tac	gag	ggc	ttc	tac	aag	cgc	ggc	ttc	ttc	gtg	acg	aag	aag	1776	
Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys	Lys		
			580					585				590					
aag	tac	gcg	gtt	ata	gac	gag	gag	gac	aag	ata	acg	acg	cgc	ggg	ctt	1824	
Lys	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Asp	Lys	Ile	Thr	Thr	Arg	Gly	Leu		
		595					600					605					
gaa	ata	gtt	agg	cgt	gac	tgg	agc	gag	ata	gcg	aag	gag	acg	cag	gcg	1872	
Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln	Ala		
	610					615					620						
agg	gtt	ctt	gag	gcg	ata	cta	aag	cac	ggc	gac	gtt	gaa	gaa	gcg	gta	1920	
Arg	Val	Leu	Glu	Ala	Ile	Leu	Lys	His	Gly	Asp	Val	Glu	Glu	Ala	Val		
625					630					635					640		
agg	att	gtc	aaa	gag	gtt	acg	gag	aag	ctg	agc	aag	tac	gag	gtt	cca	1968	
Arg	Ile	Val	Lys	Glu	Val	Thr	Glu	Lys	Leu	Ser	Lys	Tyr	Glu	Val	Pro		

Replacement Figure

645	650	655	
ccg gag aag ctg gtc atc tac gag cag ata acc cgc gac ctg aag gac Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Asp Leu Lys Asp 660 665 670			2016
tac aag gcc acc ggg ccg cat gtg gct gtt gca aaa cgc ctc gcc gca Tyr Lys Ala Thr Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala 675 680 685			2064
agg ggg ata aaa atc cgg ccc gga acg gtc ata agc tac atc gtg ctc Arg Gly Ile Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu 690 695 700			2112
aaa ggc tcg gga agg att ggg gac agg gct ata ccc ttt gac gaa ttt Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe 705 710 715 720			2160
gac ccg gca aag cac aag tac gat gca gaa tac tac atc gag aac cag Asp Pro Ala Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln 725 730 735			2208
gtt ctt cca gct gtg gag agg att ctg agg gcc ttt ggt tac cgt aaa Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys 740 745 750			2256
gaa gat tta agg tat cag aaa acg cgg cag gtt ggc ttg ggg gcg tgg Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp 755 760 765			2304
cta aaa cct aag aca tga Leu Lys Pro Lys Thr			2322

Figure 17A

Pyrococcus furiosus gene for archaeal histone (Hmf-like)
(ACCESSION No: AB013081)

Nucleotide sequence (SEQ ID NO: 63)

Amino acid sequence (SEQ ID NO: 64)

```
M M G E L P I A P V D R L I R K A G 18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54

A Q R V S E Q A A K V L A E H L E E 36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108

K A I E I A K K A V D L A K H A G R 54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162

K T V K V E D I K L A I K S * 69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA 207
```

Figure 17B

(Hmf-like)-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 64) // Amino acid sequence (SEQ ID NO: 66)

```
M M G E L P I A P V D R L I R K A G 18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54

A Q R V S E Q A A K V L A E H L E E 36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108

K A I E I A K K A V D L A K H A G R 54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162

K T V K V E D I K L A I K S 69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC
```

Replacement Figure

```

      G   G   G
      // GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   V   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG CTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTG GCC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D   L   Y   Q   L   L   S   D   R   I   H   V   L   H   P   E   G   Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G   I   G   E   K   T   A   R   K   L   L   E   E   W   G   S   L   E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

```

Replacement Figure

A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

 L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

 L E S P K A L E E A P W P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC

 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC AGG AGG GGC GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC

 G E W T E E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

 A N L W G R L E G E E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG

 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

Replacement Figure

A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC GTC CTG GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCG GCC AAG ACC ATC

 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

 K V R A W I E K T L E E G R R G Y

Replacement Figure

AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GGC AGG AGG CGG GGG TAC
 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
 T A A A D L M K L A M V K L F P R L E
 ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
 E M G A R M L L Q V H D E L V L E A
 GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
 P K E R A E A V A R L A K E V M E G
 CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG
 V Y P L A V P L E V E V G I G E D W
 GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGC ATA GGG GAG GAC TGG
 L S A K E G I D G R G G G G H H H
 CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT
 H H *
 CAT CAT TAA

Figure 17C

Taq DNA polymerase-(Hmf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 63)

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 64)

G G G
 GGC GGC GGT

 V T S G M L P L F E P K G R V L L V
 GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

Replacement Figure

D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A V Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTC GGG

L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L E V D F A K R R E P D R E R L

Replacement Figure

CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG CCG GAA GGC GCC
 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC AGG GGC GGC CTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGC CTT CTC GCC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC CCC ATG CTC CTC GCC
 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGC GTG GCC CGG CGC TAC GGC
 G E W T E E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGC GAG CGG GCC CTT TCC GAG AGG CTC TTC
 A N L W G R L E G E R L L W L Y R
 GCC AAC CTG TGG GGC AGG CTT GAG GGC GAG AGG CTC CTT TGG CTT TAC CGG
 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTC GGC CAC ATG GAG GCC ACG GGC GTG
 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
 A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC
 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGC CTT CCC GCC ATC

Replacement Figure

G K T E K T G K R S T S A A V L E A
 GGC AAG ACG AAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC GTC CTG GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG AAG AAT CTC GAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC AGC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GGC AAG ACC ATC

 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

 K V R A W I E K T L E E G R R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GGC AGG AGG CGG GGG TAC

 V E T L F G R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCC GGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

Replacement Figure

T	A	A	D	L	M	K	L	A	M	V	K	L	F	P	R	L	E	
ACC	GCC	GCC	GAC	CTC	ATG	AAG	CTG	GCT	ATG	GTG	AAG	CTC	TTC	CCC	AGG	CTG	GAG	
E	M	G	A	R	M	L	L	Q	V	H	D	E	L	V	L	E	A	
GAA	ATG	GGG	GCC	AGG	ATG	CTC	CTT	CAG	GTC	CAC	GAC	GAG	CTG	GTC	CTC	GAG	GCC	
P	K	E	R	A	E	A	V	A	R	L	A	K	E	V	M	E	G	
CCA	AAA	GAG	AGG	GCG	GAG	GCC	GTG	GCC	CGG	CTG	GCC	AAG	GAG	GTC	ATG	GAG	GGG	
V	Y	P	L	A	V	P	L	E	V	E	V	G	I	G	E	D	W	
GTG	TAT	CCC	CTG	GCC	GTG	CCC	CTG	GAG	GTG	GAG	GTG	GGG	ATA	GGG	GAG	GAC	TGG	
L	S	A	K	E	G	I	D	G	R	G	G	G	G	H	H	H	H	
CTC	TCC	GCC	AAG	GAG	GGC	ATT	GAT	GGC	CGC	GGC	GGA	GGC	GGG	CAT	CAT	CAT	CAT	
H	H	//																
CAT	CAT	//																
M	M	G	E	L	P	I	A	P	V	D	R	L	I	R	K	A	G	18
ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
A	Q	R	V	S	E	Q	A	A	K	V	L	A	E	H	L	E	E	36
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
K	A	I	E	I	A	K	K	A	V	D	L	A	K	H	A	G	R	54
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
K	T	V	K	V	E	D	I	K	L	A	I	K	S	*				69
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	TGA				

Figure 17D

Pfu DNA Polymerase (WT) -(Hmf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 61) //Nucleotide sequence (SEQ ID NO: 63)

Replacement Figure

//
ccctggtcct ggggccacat atatgttctt actcgcccttt atgaagaatc ccccgctgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctccoctat tttctctctt atgagatttt taagtatatg tatagagaag
gttttatact ccaaaactgag ttagtagata tgtgggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaaatt
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg gaaaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtcttct cggcaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaacctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaaagcc
aaaggagaag gtatacgccg acgagatagc aaagcctgg gaaagtggag agaaccttga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt

Replacement Figure

ccctccaatg gaaattcagc ttccaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaaccttg tagagtgggt cttactttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaaga aggctcaggg agagctacac
aggtaggttc gttaaagagc cagaaaaagg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctgggttt ataccaagtc tcttgggaca ttgttttagg gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaat ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctgggggaaga aagtaacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtgggttta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cactagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccagggttctt ccagcggtag ttaggatatt

Replacement Figure


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ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcaattcaa acgccttcgt tagaaaatggt
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttctgcagac gtagatcttt
tttgctcaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtcogct
acaatttttt ccttgatatc cctaattgat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt ttggaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taactttttac agaaaataact gtctcaaaatt atgacaaactc ttgacatttt tacttcatta
ccagggtaat gttttttaagt atgaaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaa taccagacga caatgggtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtttagc tcntccnnga
aagattgaga tgttcttg //
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

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Replacement Figure

Figure 17E

(Hmf-like) - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 63) //Nucleotide sequence (SEQ ID NO: 61)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

ccctggtcct ggggccacat atatgttctt actcgccctt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatatg tatagagaag
gttttatact ccaaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaaatt
taagatagag catgatagaa ctttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaggcat ggaagattg tgagaattgt
tgatgtagag aagggtgaga aaaagtttct cggcaagcct attaccgtgt ggaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gtagagaaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaacctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaag gtgattactt gaaaaaacat agatcttcca tacgttgagg ttgtatcaag

Replacement Figure

tcgtgggtta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggg
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgacc caagtcgcgt
acaatttttt ccttgtatct cctaattgat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta

Replacement Figure

cgagagagag atgataaaga gattttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaacccttga
gagagttgcc aaataactcg tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaaccttg tagagtgggt cttacttagg aaagcctacg aaagaaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaaga aggtcaggg agagctacac
aggtaggattc gttaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctgggttt ataccaagtc tcttgggaca ttgtttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaaatt ctttctacgg atattatggc tatgcaaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctgggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggatttaa agtcctctac attgacactg atggctctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac

Replacement Figure

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagctttccaa agtgggtgtt cagactttta
gacactcaa taccagacga caatggtgtg ctactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttcttgg // TGA

Figure 17F

(Hmf-like) - PFU DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 27)
Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	//				

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGGCATGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240
ACCGTGTGGA AACTTTATT GGAACATCCC CAAGATXXXC CCACATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGG AAAACATAGA TCITCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720

ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGTTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGTCCAAAC AAGCCAAAGTG AAGAGGAGTA TCAAGGAAGG 1140
 CTAGGAGAGA TGTACACAGG TGGATTCTGT AAAGGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
 ATAGATTACC CAGATTCTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAGAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAATA CATAAATTC AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAAAGCCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
 // TGA

Figure 17G

PFU DNA POLYMERASE (V93 R OR E) -(Hmf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 63)

Replacement Figure

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTTCAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTTATT GGAACATCCC CAAGATXXXC CCACATTATT AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GATTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCGAG ATGAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAATTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCACCTTAT 960
GAATCTCGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACTT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGTCCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATATCT TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTAATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAAATA CATAAATTC AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCCTTCGT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTATAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTTGGAGCA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAAATG TAAAAGAAGT AATACAAAAG CTTTGCCAAT ATGAAATTC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGCCA TTACATGAGT ATAAGGCGAT AGGTCCCTAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAAAT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220

Replacement Figure

GCGGTACTTA GGATATTGGA GGGATTTTGGA TACAGAAAAGG AAGACCTCAG ATACCAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCTGGCTT AACATTAAAA AATCC // 2328

 ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17H

PFU DNA POLYMERASE (G387P/V93R OR E) - (HMF-like) fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 63)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
 V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTATG ATGTGGATTG CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
 AAAGAGAACG GAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCITGCTTC 420
 GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCITCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
 AAAAGGCGAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGG GAAAGCCAAA GGAGAAGTGA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
 AGTGAGGAG ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCACTTAT 960
 GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAGG 1140

Replacement Figure

CTCAGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGGCG TTACTGCCCTG GGGAAAGAAA 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAA GTGAGGAAAT AAAGAAAAG 1680
 GCTCTAGAAT TTGTAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCCTTCGT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAG TCATTTACTCG TGTTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAAATC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAAGCT 1920
 GTGAGAAATAG TAAAGAGAGT AATACAAAAG CTTGCCAATT ATGAAATTTCC ACCAGAGAA 1980
 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAAGGCGAT AGTCCCTCAC 2040
 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCAAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTTCCA 2220
 GCGTACTTGA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAAG 2280
 ACAAGACAAAG TCGGCCTAAC TTCTTGCTT AACATTAAAA AATCC // 2328

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17I

(Hmf-like) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 29)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 30)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
 V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54

Replacement Figure

GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCG CAAGCCTATT 240
ACC GTGTGA AACCTTATT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGACATC CAGCGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATGCACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TC TTGCCCTT 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGGA AAAACATAGA TC TTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAAGGCAG AAAAATTTGG GATTAAATTA ACCAATTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGATACA TTTCCGACTTG 780
TATCATGTAA TAACAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGAGAGAA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCACCTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACTT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTTGTAG AGTGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAAGAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGSGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTATG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTG GGGAAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTC AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAGAGGGG ATTTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAAG CTTGCCAAT ATGAAATTC ACCAGAGAAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAAGACCA TTACATGAGT ATAGGCGAT AGGTCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAAT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TAGGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAAACCA GGTCTTTCCA 2220

Replacement Figure

GCGGTACTTA GGATATTGGA GGGATTGTGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG 2328

Figure 17J

(HMF-LIKE) -PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
 V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
 AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
 CTTCTCAGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXX CCACATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGAGATAC 360
 CTCATCGACA AAGGCCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCCTGCCCTC 420
 GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCCTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGAG 600
 AAGGATCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGACTCCC ATATTAGCG 660
 AAAAGGCGAG AAAAATCTGG GATTAAATTA ACCATTGGA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAG GAAGAATACA TTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTTT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
 GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020

Replacement Figure

TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
 CTCAGGGAGA GCTACACA GGT=GGATTTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACATAGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
 GCAAAGCAA TAGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGGAAAGAAA 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
 CTCGCAATAT ATAGCAGAT AACAGACCA TTACATGAGT ATAAGCGAT AGGTCCTCAC 2040
 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCTCTGGCTT AACATTAAAA AATCC // 2328

TGA

Figure 17K

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) - (HMF-LIKE) fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 63)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
 V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
 CTTCTCAGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240

Replacement Figure

ACCGTGTGGA AACTTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAAATGA AGCAAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCAATCCC ATATTAGCG 660
 AAAAGGCGAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATCAGAGAAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
 TATCATGTAA TACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTTG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTACAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAAGAAG 1140
 CTCAGGGAGA GCTACACA GGTGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAAATTACCCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
 GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTTG GGAAGAAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAATA CATAAAATCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAAG TCAATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGTCTCTAC 2040
 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCTGTGCTT AACATTAAAA AATCC // 2328

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
 AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
 AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Replacement Figure

Figure 17L

KOD DNA POLYMERASE - (HMF-like) fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATCCTCG ACACTGACTA CATAACCGAG GATGAAAGC CTGTCAATAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CTTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACCTTGA AGAACGTGGA TCTCCCTAC 540
GTTGACGTGC TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GGCAGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCA AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATCGAA GGTCACATAC 960
GAGCTTGGGA AGGATTCTCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAGCCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTGCCG 1260
GATACGCTCA ACGAGAAGG ATGCAAGGAA TATGACGTTG CCCACACAGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGA CAGAGCGTAA CGGCCTGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGTCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680

Replacement Figure

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ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACCGGCTTT CTTGTCACG AAGAAGAAGT ATGCGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCTGTC TCAAGGGCTC TGGGAGGATA GGCACACAGG CGATACCCTT CGACGAGTTC 2160
GACCCGACGA AGCAAAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325
//
    ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
    GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
    AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
    AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

```

Figure 17M

(Hmf-like) - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

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ATGATCCTCG ACACGTGACTA CATAACCGAG GATGGAAAGC CTGTCTATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAG GTTCAGAAGA AGTTCTCGG GAGACCAAGT 240
GAGGTCTGGA AACTTACTT TACTATCCG CAGGACXXXC CAGGATTAAG GGACAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCG CAAGCGTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCACGAGG AGCTGAAAAT GCTCGCCTTC 420

```

Replacement Figure

GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGAA GGGATGGAAG CGAGCCGAAG 720
ATTGAGAGGA TGGGCGACAG GTTTGCCGTC GAAAGTGAAG GACGGATACA CTTGATCTC 780
TATCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCCAC AGCCTGGGA 900
ACCGTTGGA AGGATGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
GAGCTGGGA AGGATGCTT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAA CAGCCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGTGCCA AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACCGGCTT CTTCTGTCAG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAGGACG GTGACGTGCA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCNAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG ACGAGATAAC GAGGGAATTA AAGGACTACA AGGCAACCCG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAAGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTGCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17N

(Hmf-like)-Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 36)

Replacement Figure

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) ;

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT	54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA	108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA	162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //	

ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG	60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCCTCATT TTCAGCCCTA TATATATGCT	120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCCA TAAAGGGCGA GAGACATGGA	180
AAAACGTGTA GAGTGTGCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT	240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA	300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCTTTTGC CAAGCGTTAT	360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT	420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGAA AGGGCGAGAT AATAATGATT	480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCAGATGGA AAAATATCGA TTITGCCGTAT	540
GTGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA	600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCAT	660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA	720
CCCAAGATTG AGAGGATGGG TGATAGTTTT GCTGTGAAAA TCAAGGGTAG AATCCACTTT	780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT	840
TATGAAGCAG TTTTATGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA	900
TGGGAACACG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGGCA	960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT	1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA	1080
AGGGTGGCAT ACGCGAGGAA TGAACCTTGA CCGAACAAAC CTGATGAGGA AGAGTATAAA	1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG	1200
GAATAATCA TTTATTTGGA TTTCCGCAGT CTGTACCCCTT CAATAATAGT TACTCACAA	1260
GTATCCCCAG ATACCTTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA	1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATCTCGG GGACTTAATT	1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA	1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG	1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG	1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT	1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA	1680
AAGAAAAGCCA AGGAATTCCT AAACCTACATA AACCTCCAAAC TTCCAGGTCT GCTTGAGCTT	1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA	1800
GATGAAGAGG GCAGGATAAC AACAAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG	1860

Replacement Figure

ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACATT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTG CGATAGCAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
 ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
 ACAGAAATACG ATCTTAGAAA ACACAAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 170

Vent DNA POLYMERASE - (Hmf-like) FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
 AAAGAGAACG GGGAGTTTAA ATAGAACTT GACCTCATT TTCAGCCCTA TATATATGCT 120
 CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
 AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
 GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
 AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
 CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
 GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
 AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACAATGA AAAATATCGA TTTGCCGTAT 540
 GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
 AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCAT 660
 AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
 CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
 GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
 TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
 TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
 ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
 CAAAGTGAT TGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
 AGGTTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
 CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAG AGCCAGAAAA AGGTTTGTGG 1200

Replacement Figure

GAATAATCA TTTATTTGGA TTTCCGCAGT CTGTACCCCTT CAATAATAGT TACTACAAC 1260

GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320

GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACCTCGG GGACTTAATT 1380

GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440

ATGCTCGATT ATAGGCAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500

GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560

AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620

TATCGGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680

AAGAAAGCCA AGGAATTCTT AAATACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740

GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800

GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860

ATAGCTAAGG AGACTCAGG AAAGTTTTTA GAGGCTATAC TTAAGAGAGG AAGTGTTGAA 1920

AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACATT 1980

GAAGAAGCTG TTATCCATGA GCAGATTACC AGGGAATTAA AGGACTACAA AGCCATTGGC 2040

CCTCATGTG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100

ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGAGATA GCGATAGGTT AATTTTACTT 2160

ACAGAATACG ATCTAGAAA ACACAAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220

TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280

CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54

GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108

AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162

AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17P

Deep Vent- (Hmf-like) DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 63)

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60

AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120

CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGG 180

AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCTTGG GAGGCCGATT 240

GAGGTATGGA GGCTGTACTT TGAACACCCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300

AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCCG GAAGAGGTAC 360

Replacement Figure

CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCCTCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720
ATGCAGAGTG	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAGACCAAA	GGAGAAAGTT	TACGCTACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAGG	GACTGGAGAG	AGTTGCAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCCT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACCTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAACACAGT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACCTGGAG	GAAAAGTTTCG	GGTTCAAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCCCT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATT	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGATAG	TTAAGGAGGT	AAC TGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCAAGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG //		2328

ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	TGA				

Figure 17Q

Replacement Figure

(EMflike) - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT 54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA 108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA 162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
CTCCTCAAAG ATGATCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCAAT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC 360
CTAATAGACA AAGGCCTAAT TCCAATGGA GGCATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACAAC GCGGATTTCT TCGACCTTCC CTATCTAGTT 660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG 840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCAG AGATAGCTGA GGCCTGGGAG 900
ACTGGAAGG GACTGGAGAG AGTTGCAAAG TATTTCAATGG AGGATGCAA GGTAAACGTAC 960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTCCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGATACGC TGAACAGGGA AGGCTGTAGG CCAACGCTGC TCGCCCCAGA GGTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGTTTATC CCCAGCTGTC TCAAGAGGTT ATTGGATGAA 1380
AGGCAAGAAA TAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA 1560

Replacement Figure

TATATAGAGT	TCGTAAGGAA	GGAAGTGGAG	GAAAAGTTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAAATTCCT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGCTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAAGT	CCTAGAGGCT	ATCCTAAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGAGTAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAAGGCTAT	AGGTCCGCAC	2040
TTGTCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGG	AGACGGGCCA	ATAAGCAAGA	GGCTATCTCT	TGCAGAGGAG	2160
TTTCATCTCA	GGAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17R

JDF-3 - (Hmf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 63)
 Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT
 ACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGTTAAGCCGCGGAGAAAGGTGAAGAAAAGTTCTCTCGG
 CAGGTCGTGGAGGTCGTGGTCCCTCTACTTCACGCACCCGCGAGGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGGTCAATCGACATCTACGAGTACGACATACCC
 TTCGCCAAGCGTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTGGAGATCGAGACCGCTTACCCAGGGAGAAAGAGTTTGGAA
 CCGGGCCGATTCTGATGATAAGCTACGCCGATGAAGCGAGGCGCGGTGATAACCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAGGAGATGATTA
 GCGTCTTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGTGATAACATACAAACGGCGACAACCTTCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTT
 ACCCTCGGAGGGAACGGAGCGAGCCGAAGATACAGCGCATGGGGGACAGGTTTTCGGTTCGAGGTGAAGGCGAGGTACCCAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGCTTGAGAG
 ACCTCCGACCTACACCTTGAGGCTGTATAACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCGAGGAGTACCCAGGAGAGTACCGCTGGGAGACCGGCGAGGGCTTGAGAG
 GGTCCGCGCTACTCGATGGAGGACCGAGGGTTACTACGAGCTTGGCAGGAGTCTTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCC
 CGTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCTTAAGGAAGCCCTACGAGAGGAACGAACCTCGTCCCAACAGCCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGCT
 ACgCGGTGGCTACGTCAAGGACCGGAGCGGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCTCAATCATATAATCACCCACAACGTCTCGCCAGATAC
 GCTCAACCGCGAGGGGTGATGAGACTACGACGTTTGGCCCGAGGTGGTCAAGTTCTGCAAGGAATTCCTCCCGGCTTCAATCCGAGCTTCCGAAAACCTGCTGGAGGAAAGG
 CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCTCGATTACAGGCAACGGGCTATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
 ATGCCAGGGCAAGATGGTACTGCAGGGAGTGGCCGAGAGCGTTACGGCATGGGAAGGGAGTACATCGAAATGGTTCATCAGAGAGCTTGAGGAAAAGTTCCGTTTAAAGTCTC
 CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCTTCTC
 GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACCGCGGTCTATCGACGAGGAGGGCAAGATAACCAACGCGCGGGCTTGAGATAGTCAGGCGG

ACTGGAGCGAGATAGCGAAGGAGACGCGAGGCGAGGGTTTTGGAGGGCGATACTCAGGCACGGTGACGTTGAAGAGGGCCGTCAGAATTGTACAGGAAGTCAACCGAAAAGCTGAGCAA
GTACGAGGTTCCGCGGAGAGACTGGTTATCCACGAGCAGATAACGCGGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAGcGTTTGGCCCGCAGAGGT
GTTAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATG
CGGACTACTACATCGAAGAACCAAGTTCTGCCGCGAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTCGGCTACCGAAGACGAGGCAAGTCTGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGAAGAAG//

ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	TGA				

Figure 17S

(Hmf-1like) - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG	ATG	GGA	GAA	TTA	CCA	ATT	GCC	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	54
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CTT	GCA	GAG	CAC	CTT	GAG	GAA	108
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	162
AAG	ACC	GTT	AAG	GTC	GAA	GAC	ATT	AAG	CTC	GCA	ATT	AAG	AGC	//				

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAGCCCGTCAATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAGCC
CTACTTCTACGCGTCTCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAAACCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGGAGAAAGTGA
AGAAAAGTTCTCTCGCAGGTCTGTGAGGTCTGGGTCTCTACTTACGCACCCGACGACXXXCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGGGTCATC
GACATCTACGAGTACGACATACCTTCGCCAAGCGTACCTCATAGACAAGGGCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTCTGACGATCGA
GACGCTCTACACGAGGGAGAAGAGTTTGGAAACCGGGCCGATTCTGTATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATAACCTGGAAGAAGATCGACCTTC
CTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAAGCGTCTTTGAGGGTCTTTAAGGAGAAGGACCCGGACGTGTGATAACATAACAACGGCGACAACCTTC
GACTTCGCTACCTGAAAAAGCGTGTGAGAAGCTTTGGGTGAGCTTTTACCTCGGAGGAGACGGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTGGGT
CGAGTGAAGGCGAGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAACTCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGC
CCAAGGAAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGCTTGAGAGGGTCCGCGCTACTCGATGGAGGACCGGAGGGTTACCTACGAG
CTTGGCAGGGAGTTCTTCCGATGGAGGCCAGCTTCCAGGCTCATCGGCCAAGGCTCTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCTCT
CCTAAGGAAGGCCCTACGAGAGGAAAGAACTCGTCTCCCAACGAGCCCGAGAGGGAGCTGGCGAGGAGAAGGGGGGCTACgcCGGTGGCTACGTCAAGGAGCCGG
AGCGGGGACTGTGGGACAAATATCGTGTATCTAGACTTTCGTAGTCTCTACCTTCAATCAATAATCACCCACAACGTCTCGCCAGATACGCTCAACCCGAGGGGTGT
AGGAGCTACGACGTTGGCCCCCGAGGTCGGTCAACAAGTTCTGCAAGGACTTCCCCGGCTTCATTCGGAGCCCTGCTCGGAAACCTGCTGGAGGAAGGCAAGATATAA

GAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAAGAAATCTCTCGATTACAGGCAACGCGCCATCAAGATTCTCGCCAA CAGCTACTACGGCTATG
CCAGGGCAAGATGGTACTG CAGGGAGTGC GCCCGAGAGCGTTTACGGCATGGGGAAGGGAGTACATCGAAATGGTTCATCAGAGAGCTTGAGGAAAAAGTTTCGGTTTTAAA
GTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAA
GCCCCGCCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAAGGGGCTTCTCGTCA CGAAGAAAAAGTACGCGGTCTCGACGAGGAGGGCAAGATAACCCACGCGCG
GGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGCAGGCGAGGGTTTGGAGGCGGATACTCAGGCA CGGTGACGTTGAAGAGGCCCGTCAGAA
GTCAGGGGAAGTCAACCGAAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGAAAGCTGGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGACTACAAGGCCACCCGCCCC
GCACGTAGCCCATAGCGAAAGCGTTTGGCCGCCAGAGGTGTTAAAAATCCGGCCCCGGAACGTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAAGGATAGGCGACAGGG
CGATTCCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCCAGGTTCTGCCGGCAGTTGAGAGAAATCCCTCAGGGCCCTTCGGC
TACCGCAAGGAAGACCTTGCCTAC CAGAAGACGAGGCAGGTCGGGCTTGGCGCGTGGCTGA

Replacement Figure

Figure 17T

Pyrococcus furiosus DSM 3638, Archaeal histone (Hmf-1) section 85 of 173 of the complete genome.
ACCESSION No: AE010210 REGION: complement (8333..9082)
/product="pcna sliding clamp (proliferating-cell nuclear antigen)"

Nucleotide sequence (SEQ ID NO: 67)

Amino acid sequence (SEQ ID NO: 68)

M	P	F	E	I	V	F	E	G	A	K	E	F	A	Q	L	I	D	18
ATG	CCA	TTT	GAA	ATC	GTA	TTT	GAA	GGT	GCA	AAA	GAG	TTT	GCC	CAA	CTT	ATA	GAC	54
T	A	S	K	L	I	D	E	A	A	F	K	V	T	E	D	G	I	36
ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
S	M	R	A	M	D	P	S	R	V	L	I	D	L	N	L	P		54
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CTC	CCG	162
S	S	I	F	S	K	Y	E	V	V	E	P	E	T	I	G	V	N	72
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC	216
M	D	H	L	K	K	I	L	K	R	G	K	A	K	D	T	L	I	90
ATG	GAC	CAC	CTA	AAG	AAG	ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG	GAC	ACC	TTA	ATA	270
L	K	K	G	E	E	N	F	L	E	I	T	I	Q	G	T	A	T	108
CTC	AAG	AAA	GGA	GAG	GAA	AAC	TTC	TTA	GAG	ATA	ACA	ATT	CAA	GGA	ACT	GCA	ACA	324
R	T	F	R	V	P	L	I	D	V	E	E	M	E	V	D	L	P	126
AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG	GAA	GTT	GAC	CTC	CCA	378
E	L	P	F	T	A	K	V	V	V	L	G	E	V	L	K	D	A	144
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	GTT	CTT	GGA	GAA	GTC	CTA	AAA	GAT	GCT	432
V	K	D	A	S	L	V	S	D	S	I	K	F	I	A	R	E	N	162

Replacement

Figure

GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
E F I M K A E G E T Q E V E I K L T	180
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
L E D E G L L D I E V Q E E T K S A	198
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
Y G V S Y L S D M V K G L G K A D E	216
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
V T I K F G N E M P M Q M E Y Y I R	234
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
D E G R L T F L L A P R V E E *	250
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA	750

Figure 17U

(PCNA)-Tag DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 65)
Amino acid sequence (SEQ ID NO: 68) // Amino acid sequence (SEQ ID NO: 66)

M P F E I V F E G A K E F A Q L I D	18
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
T A S K L I D E A A F K V T E D G I	36
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
S M R A M D P S R V V L I D L N L P	54
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162

Replacement

Figure

GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTC GTG
 D G H H L A Y R T F H A L K G L T T
 GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC
 S R G E P V Q A V Y G F A K S L L K
 AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG
 A L K E D G D A V I V F D A K A P
 GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG TTT GAC GCC AAG GCC CCC
 S F R H E A Y G G Y K A G R A P T P
 TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC GCC CCC ACG CCA
 E D F P R Q L A L I K E L V D L L G
 GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTC GGG
 L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTC GGC AGC CTG
 A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
 D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC
 L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG
 A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

Replacement

Figure

A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

 L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

 L E S P K A L E E A P W P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC

 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

 L A A A R G G R V H R A P E P Y K A
 CTG GCC GCC AGG GGC GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

 L R D L K E A R G L L A K D L S V L
 CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC

 G E W T E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

 A N L W G R L E G E E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG

 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

Replacement

Figure

A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC GTC CTG GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GGC GCC AAG ACC ATC

 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I P Y E E A Q A F I E R Y F Q S F P

Replacement

Figure

ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
 K V R A W I E K T L E E G R R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GGC AGG AGG CGG GGG TAC
 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCC GCG ATG GGC TTC AAC ATG CCC GTC CAG GGC
 T A A D L M K L A M V K L F P R L E
 ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
 E M G A R M L L Q V H D E L V L E A
 GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
 P K E R A E A V A R L A K E V M E G
 CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG
 V Y P L A V P L E V E V G I G E D W
 GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
 L S A K E G I D G R G G G G G G H H H
 CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC CAT CAT CAT CAT
 H H *
 CAT CAT TAA

Figure 17V

Taq DNA polymerase- (PCNA) fusion protein

Replacement

Figure

Nucleotide sequence (SEQ ID NO: 65) /Nucleotide sequence (SEQ ID NO: 67)
Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 68)

G G G
// GGC GGC GGT

V T S G M L P L F E P K G R V L L V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A V Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

Replacement

Figure

A N L W G R L E G E E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG

 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

 A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC CTC CTG GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F

Replacement

Figure

CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC
 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
 K V R A W I E K T L E E G R R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC
 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCC GCG GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
 T A A D L M K L A M V K L F P R L E
 ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
 E M G A R M L L Q V H D E L V L E A
 GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
 P K E R A E A V A R L A K E V M E G
 CCA AAA GAG AGG GCG GAG GCC GTG GCC CTG GCG AAG GAG GTC ATG GAG GGG
 V Y P L A V P L E V E V G I G E D W
 GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
 L S A K E G I D G R G G G G H H H
 CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT
 H H //
 CAT CAT //

Replacement

Figure

M	P	F	E	I	V	F	E	G	A	K	E	F	A	Q	L	I	D	18
ATG	CCA	TTT	GAA	ATC	GTA	TTT	GAA	GGT	GCA	AAA	GAG	TTT	GCC	CAA	CTT	ATA	GAC	54
T	A	S	K	L	I	D	E	A	A	F	K	V	T	E	D	G	I	36
ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
S	M	R	A	M	D	P	S	R	V	V	L	I	D	L	N	L	P	54
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CTC	CCG	162
S	S	I	F	S	K	Y	E	V	V	E	P	E	T	I	G	V	N	72
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC	216
M	D	H	L	K	K	I	L	K	R	G	K	A	K	D	T	L	I	90
ATG	GAC	CAC	CTA	AAG	AAG	ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG	GAC	ACC	TTA	ATA	270
L	K	K	G	E	E	N	F	L	E	I	T	I	Q	G	T	A	T	108
CTC	AAG	AAA	GGA	GAG	GAA	AAC	TTC	TTA	GAG	ATA	ACA	ATT	CAA	GGA	ACT	GCA	ACA	324
R	T	F	R	V	P	L	I	D	V	E	E	M	E	V	D	L	P	126
AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG	GAA	GTT	GAC	CTC	CCA	378
E	L	P	F	T	A	K	V	V	V	L	G	E	V	L	K	D	A	144
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	GTT	CTT	GGA	GAA	GTC	CTA	AAA	GAT	GCT	432
V	K	D	A	S	L	V	S	D	S	I	K	F	I	A	R	E	N	162
GTT	AAA	GAT	GCC	TCT	CTA	GTG	AGT	GAC	AGC	ATA	AAA	TTT	ATT	GCC	AGG	GAA	AAT	486
E	F	I	M	K	A	E	G	E	T	Q	E	V	E	I	K	L	T	180
GAA	TTT	ATA	ATG	AAG	GCA	GAG	GGA	GAA	ACC	CAG	GAA	GTT	GAG	ATA	AAG	CTA	ACT	540
L	E	D	E	G	L	L	D	I	E	V	Q	E	E	T	K	S	A	198
CTT	GAA	GAT	GAG	GGA	TTA	TTG	GAC	ATC	GAG	GTT	CAA	GAG	GAG	ACA	AAG	AGC	GCA	594
Y	G	V	S	Y	L	S	D	M	V	K	G	L	G	K	A	D	E	216
TAT	GGA	GTC	AGC	TAT	CTC	TCC	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	GCC	GAT	GAA	648

Replacement

Figure

V	T	I	K	F	G	N	E	M	P	M	Q	M	E	Y	Y	I	R	234
GTT	ACA	ATA	AAG	TTT	GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	GAG	TAT	TAC	ATT	AGA	702
D	E	G	R	L	T	F	L	L	A	P	R	V	E	E	*			250
GAT	GAA	GGA	AGA	CTT	ACA	TTC	CTA	CTG	GCT	CCA	AGA	GTT	GAA	GAG	TGA			

Figure 17W

Pfu DNA Polymerase (WT) -(PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 67)

```

ccctggtcct gggtcacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt
taagatagag catgatagaa ctttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg gaaaaggcat ggaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtctct cggcaagcct attaccgtgt gaaaacttta
tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaggcct

```

Replacement

Figure

aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaag gtgattactt ggaaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaagcctgg gaaagtggag agaacccttga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtgggt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaaga aggcctcagg agagctacac
aggtaggattc gttaaagagc cagaaaaagg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagtctt gcaaggacat
ccctggtttt ataccaagtc tcttgggaca ttgttttagg gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaat ctttctacgg atattatggc tatgcaaaaag caagatggta

Replacement

Figure

ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggatttaa agtcctctac attgacactg atggctctcta
tgcaactatc ccaggaggag aaagtgagga aataaaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaattt gcaaaagaaa ctcaagctag
agttttggag acaataactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cactagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatat acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac tttattctt
tctaaccttt ttctatgaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatgggt
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct

Replacement

Figure

```

tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttccgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgacc caagtcogct
acaatttttt ccttgatatc cctaattgtat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt ttggaatcct ttaactctgg
aaagtataat ttcaagctcc ttctttcttca tgacagatga aaaattgttt tgtctctttt
taactttttac agaaaataact gtctcaaaatt atgacaaactc ttgacatttt tacttcatta
ccagggtaat gttttttaagt atgaaaatttt tcctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagacttttta
gacactcaaa taccagacga caatgggtgtg ctactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntccnga

aagattgaga tgttcttgg //
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA TAT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

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Replacement

Figure

Figure 17X

(PCNA) - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 61)

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG
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ccctggctct ggggccacat atatgttctt actgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggtattc aaaaaagaga acgaaaaatt
```

Replacement

Figure

taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg gaaaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta
tttggaaacat cccaagatg ttcccactat tagagaaaaa gttagagAAC atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaaag gtgattactt ggaaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccctga
gagagttgcc aaatactga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaaga aggctcaggg agagctacac
agggtgattc gttaaagagc cagaaaaagg gttgtgggaa aacatagtat acctagattt

Replacement

Figure

tagagcccta tatccctcga ttataattac ccacaatggt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc ctigactata gacaaaaagc
gataaaactc ttagcaaat ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaaagt ttggattttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataaagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaattt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cactagctg ttgcaaaaga
actagctgct aaaggagtta aaataaaagcc aggaatggta attggatata tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt

Replacement

Figure

tctaacccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggg
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa ttgcgacgac gtagatcttt
tttgctcaa gcagagccgc tccaatggat aacacccctg ttcccgacc caagtccgct
acaatttttt ccttgatat cttaatgtat aagcaagcca agggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt ttggaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataaact gtctcaaat atgacaaactc ttgacatttt tacttcatta
ccagggtaat gtttttaagt atgaaatttt tctttcatag agggagnnnn nngtcctctc
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaa taccagacga caatgggtgtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtttagc tcntccnga
aagattgaga tgttcttgg // TGA

Figure 17Y

Replacement

Figure

(PCNA) - PFU DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 27)

Nucleotide sequence (SEQ ID NO: 67) //Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC      54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA      108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG      162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC      216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA      270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA      324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA      378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT      432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT      486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT      540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA      594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA      648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA      702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
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ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAAATTTAA GATAGAGCAT GATAGAACCTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTTCAA GATTGAAGAA GTTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAAG GTTGAGAAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTGTC AAAGAGATAC 360
CTCATCGACA AAGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAGGTG ATTACTTGGG AAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
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Replacement

Figure

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AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCAATCCC ATATTTAGCG 660
AAAAGGCAG AAAAACCCTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
AGTGGAGAGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT AACCTTGTAG AGTGGTTCTT ACITTAGGAAA 1080
TTATGGGATG TTTCAAGGTC AAGCACAGGG AAGCTCCAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAGAG 1140
GCCTACGAAA GAAACGAAGT AGCTCCAAC AGCTCAAGT AAGAGGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
CTCAGGGAGA GCTACACAGG TGGATTCTGT AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
ATAGTATACC TAGATTTTAG GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
CCGATACTC TAAATCTTGA AGGATGCAAG TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1440
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1500
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTTCTT TCTACGGATA TTATGGCTAT 1560
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGAAGAGAAAG 1620
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1680
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1740
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1800
GAAGGTTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1860
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1920
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1980
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 2040
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2100
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2160
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2220
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2280
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2328
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
// TGA

```

Figure 17Z

PFU DNA POLYMERASE (V93 R OR E) -(PCNA) fusion protein

Replacement

Figure

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 67)
 Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
 AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TC TTGCCCTTC 420
 GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAAATGA AGCAAAAGTG ATTACTTGGA AAAACATAGA TC TTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTAGCG 660
 AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGACAGATA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAAATCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTC AAGGTC AAGCACAGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
 CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCCGATATC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGC AAAAGCGAT AAAACTCTTA GCAAATCTTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCGCTG GGAAGAAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG GTCCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800

Replacement

Figure

GAAGGAAAAG	TCATTACTCG	TGGTTTtagag	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860
AAAGAAATC	AAGCTAGAGT	TTTTGGAGACA	ATACTAAAAAC	ACGGAGATGT	TGAAGAAGCT	1920
GTGAGAATAG	TAAAAGAAGT	AATACAAAAG	CTTGCCCAATT	ATGAAATTCC	ACCAGAGAAG	1980
CTCGCAATAT	ATGAGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGGTCCTCAC	2040
GTAGCTGTTG	CAAGAAACT	AGCTGCTAAA	GGAGTTAAAA	TAAAGCCAGG	AATGGTAATT	2100
GGATACATAG	TACTTAGAGG	CGATGGTCCA	ATTAGCAATA	GGGCAATTCT	AGCTGAGGAA	2160
TACGATCCCA	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GGTCTCTCCA	2220
GCGGTACTTA	GGATATTGGA	GGGATTGGGA	TACAGAAAAG	AAGACCTCAG	ATACCAAAAG	2280
ACAAGACAAG	TCGGCCTAAC	TTCTCTGGCTT	AACATTAAAA	AATCC //		2328
ATG CCA	TTT GAA	ATC GTA	TTTT GAA	GGT GCA	AAA GAG	TTT GCC CAA CTT ATA GAC 54
ACC GCA	AGT AAG	TTA ATA	GAT GAT	GAG GCC	GCG TTTT	AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG	AGG GCC	ATG GAT	CCA AGT	AGA GAT	GTT GTC	CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC	ATA TTT	AGC AAA	TAT GAA	GTT GAT	GAA CCA	GAA ACA ATT GGA GTT AAC 216
ATG GAC	CAC CTA	AAG AAG	ATC CTA	AAG AGA	GGT AAA	GCA AAG GAC ACC TTA ATA 270
CTC AAG	AAA GGA	GAG GAA	AAC TTC	TTA GAG	ATA ACA	ATT CAA GGA ACT GCA ACA 324
AGA ACA	TTT AGA	GTT CCC	CTA ATA	GAT GAT	GTA GAA	GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT	CCA TTC	ACT GCA	AAG GTT	GTA GTT	GTA GAT	CTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA	GAT GCC	TCT CTA	GTG AGT	GAC AGC	ATA AAA	TTT ATT GCC AGG GAA AAT 486
GAA TTTT	ATA ATG	AAG GCA	GAG GGA	GAA ACC	CAG GAA	GTT GAG ATA AAG CTA ACT 540
CTT GAA	GAT GAG	GGA TTA	TTG GAC	ATC GAG	GTT CAA	GAG GAG ACA AAG AGC GCA 594
TAT GGA	GTC AGC	TAT CTC	TCC GAC	ATG GAT	GTT AAA	GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA	ATA AAG	TTT GGA	AAT GAA	ATG CCC	ATG CAA	ATG GAG TAT TAC ATT AGA 702
GAT GAA	GGA AGA	CTT ACA	TTC CTA	CTG GCT	CCA AGA	GTT GAA GAG TGA

Figure 17AA

PFU DNA POLYMERASE (G387P/V93R OR E)-(PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 67)

Replacement

Figure

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTATTATG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CAATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTTATTT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCCTGCCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCCTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTTAGCG 660
AAAAGGGCAG AAAAATTTGG GATTAAATTA ACCATTGGAA CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAG GAAGAATACA TTTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGATG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGTCCAAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTATG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTCG GGAAGAAGAA 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCCAATT ATGAAATTTCC ACCAGAGAAG 1980

Replacement

Figure

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CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCTGGCTT AACATTAAAA AATCC // 2328

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

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Figure 17BB

(PCNA) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 29)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 30)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

Replacement

Figure

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GAT CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	216
ATG GAC CAC CTA AAG AAG ATC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAT GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	
ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTATTATAG GCTATTCAAA 60	
AAAGAGAACG GAAATTTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120	
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180	
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCG CAAGCCTATT 240	
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300	
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360	
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCCTGCCCTTC 420	
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480	
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGGA AAAACATAGA TCCTCCATAC 540	
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600	
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCTC ATATTTAGCG 660	
AAAAGGCGAG AAAAATCTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720	
ATGCAGAGAA TAGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780	
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840	
GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900	
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960	
GAACTCGGGA AAGAATTCTT TCCAATGGA ATTTCAGCTTT CAAGATTAGT TGGACAACCT 1020	
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGTTCTTT ACTTAGGAAA 1080	
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140	
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGTT GTGGGAAAAC 1200	
ATAGTATACC TAGATTTTAT AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260	
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320	

Replacement

Figure

AAGTTCCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCGCTG GGAAGAGAA 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAGAAGTTG GATTTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAATC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGAGAGTGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGCGGAT AGTCCCTCAC 2040
 GTAGCTGTTG CAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCTTGCTT AACATTAAAA AATCC //TAG 2328

Figure 17CC

(PCNA) -PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
 V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216

Replacement

Figure

ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
 CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
 AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
 GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
 GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
 GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
 CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
 TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
 GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
 CTTCTCAGG ATGATTCAA GATTGAAGAA GTTAAGAAA TAACGGGGA AAGGCATGA 180
 AAGATTGTGA GAATTGTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240
 ACCGTGTGA AACTTTATT GGAACATCCC CAAGATXXX CCACTATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTT GAATACGATA TTCCATTTC AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
 GCNATAGCNA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGTG ATTACTTGA AAAACATAGA TCITCCATAC 540
 GTTGAGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTTAAT GGAGACTCAT TCGCATTCCT ATATTTAGCG 660
 AAAAGGGCAG AAAACCTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAG GAAGAATACA TTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCT CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGGA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
 GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
 CTCAGGGAGA GCTACACA GTT_GGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCCGATATC TAAATCTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620

Replacement

Figure

GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGRAAATC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GTATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TAGCATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
TGA

Figure 17DD

PFU DNA POLYMERASE(D141A/E143A/V93R OR E) - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 67)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAA GATTGAGAA GTTAAGAAA TAACGGGGA AAGGCATGGA 180
AAGATTGGA GAATTGTTGA TGTAGAGAAG GTTGAGAAA AGTTTCTCG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCC CAAGATXXXC CCACTATTAG AGAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTC AAAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAGAGAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480

Replacement

Figure

AGTTATGCAG	ATGAAAATGA	AGCAAAGGTG	ATTACTTTGGA	AAAACATAGA	TCTTCCATAC	540
GTTGAGGTTG	TATCAAGCGA	GAGAGAGATG	ATAAAGAGAT	TTCTCAGGAT	TATCAGGGAG	600
AAGGATCCTG	ACATTATAGT	TACTTATAAT	GGAGACTCAT	TCGCATTTCC	ATATTTAGCG	660
AAAAGGGCAG	AAAAACTTGG	GATTAAATTA	ACCATTTGAA	GAGATGGAAG	CGAGCCCAAG	720
ATGCAGAGAA	TAGGCGATAT	GACGGCTGTA	GAAGTCAAGG	GAAGAATACA	TTTCGACTTG	780
TATCATGTAA	TAAACAAGGAC	AATAAATCTC	CCAACATACA	CAC TAGAGGC	TGTATATGAA	840
GCAATTTTGT	GAAAGCCAAA	GGAGAAGGTA	TACGCCGACG	AGATAGCAA	AGCCTGGGAA	900
AGTGGTAGAG	ACCTTGAGAG	AGTTGCCAAA	TACTCGATGG	AAGATGCAAA	GGCAACTTAT	960
GAACTCGGGA	AAGAATTCCT	TCCAATGGAA	ATTCAGCTTT	CAAGATTAGT	TGGACAACCT	1020
TTATGGGATG	TTTCAAGGTC	AAGCACAGGG	AACCTTTGTAG	AGTGGTTCTT	ACTTAGGAAA	1080
GCCTACGAAA	GAAACGAAGT	AGCTCCAAAC	AAGCCAAAGT	AAGAGGAGTA	TCAAAGAAGG	1140
CTCAGGGAGA	GCTACACA	GTT_GGATTCGTT	AAAGAGCCAG	AAAAGGGGTT	GTGGGAAAAC	1200
ATAGTATACC	TAGATTTTAG	AGCCCTATAT	CCCTCGATTA	TAATTACCCA	CAATGTTTCT	1260
CCCGATATCT	TAAATCTTGA	GGGATGCAAG	AAC TATGATA	TCGCTCCTCA	AGTAGGCCAC	1320
AAGTTCTGCA	AGGACATCCC	TGGTTTATA	CCAAGTCTCT	TGGGACATTT	GTTAGAGGAA	1380
AGACAAAAGA	TTAAGACAAA	AATGAAGGAA	ACTCAAGATC	CTATAGAAA	AATACTCCTT	1440
GACTATAGAC	AAAAAGCGAT	AAAAC TCTTA	GCAAATCTTT	TCTACGGATA	TTATGGCTAT	1500
GCAAAAGCAA	GATGGTACTG	TAAGGAGTGT	GCTGAGAGCG	TTACTGCCCTG	GGGAAGAAAAG	1560
TACATCGAGT	TAGTATGGAA	GGAGCTCGAA	GAAAAGTTTG	GATTTAAAGT	CCTCTACATT	1620
GACACTGATG	GTCTCTATGC	AAC TATCCCA	GGAGGAGAAA	GTGAGGAAAT	AAAGAAAAAG	1680
GCTCTAGAAT	TTGTAAAAATA	CATAAATTCA	AAGCTCCCTG	GACTGCTAGA	GC TTGAATAT	1740
GAAGGGTTTT	ATAAGAGGGG	ATTCTTTCGTT	ACGAAGAAGA	GGTATGCAGT	AATAGATGAA	1800
GAAGGAAAAG	TCATTACTCG	TGGTTTATAG	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860
AAAGAAACTC	AAGCTAGAGT	TTTGGAGACA	ATACTAAAAC	ACGGAGATGT	TGAAGAAGCT	1920
GTGAGAATAG	TAAAAGAAGT	AATACAAAAG	CTTGCCCAATT	ATGAAATTTCC	ACCAGAGAAG	1980
CTCGCAATAT	ATAGGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGGTCCTCAC	2040
GTAGCTGTTG	CAAGAAGAACT	AGCTGCTAAA	GGAGTTAAAA	TAAAGCCAGG	AATGGTAAIT	2100
GGATACATAG	TACTTTAGAG	CGATGGTCCA	ATTAGCAATA	GGGCAATTCT	AGCTGAGGAA	2160
TACGATCCCA	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GGTTCTTTCCA	2220
GCGGTACTTA	GGATATTGGA	GGGATTTGGA	TACAGAAAAG	AAGACCTCAG	ATACCAAAAAG	2280
ACAAGACAAG	TCGGCCTAAC	TTTCTGGCTT	AACATTTAAA	AATCC //	2328	

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324

Replacement

Figure

AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA	

Figure 17EE

KOD DNA POLYMERASE - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 67)

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATCCTCG ACCTGACTA CATAACCGAG GATGGAAAGC CTGTCAATAAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCTTCGG GAGACCAGTT 240
GAGGTCCTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTGCGCG AGGGGCCAAT CTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCTAC 540
GTTGACGTG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGACAAC TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTGAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTGATCTC 780
TATCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCCTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCCG TACTCGATGG AAGATGCGAA GGTCACATAC 960

Replacement

Figure

GAGCTTGGGA	AGGAGTTTCCT	TCCGATGGAG	GCCCAGCTTT	CTCGTTTAAT	CGGCCAGTCC	1020
CTCTGGGACG	TCTCCCGCTC	CAGCACTGGC	AACCTCGTTG	AGTGTTTCCT	CCTCAGGAAG	1080
GCCTATGAGA	GGAATGAGCT	GGCCCCGAAC	AAGCCCGATG	AAAAGGAGCT	GGCCAGAGA	1140
CGGCAGAGCT	ATGAAGGAGG	CTATGTAAAA	GAGCCCGAGA	GAGGGTTGTG	GGAGAACATA	1200
GTGTACCTAG	ATTTTATGATC	CCTGTACCCC	TCAATCATCA	TCACCCACAA	CGTCTCGCCG	1260
GATACGCTCA	ACAGAGAAGG	ATGCAAGGAA	TATGACGTTG	CCCCACAGGT	CGGCCACCGC	1320
TTCTGCAAGG	ACTTCCCAGG	ATTTATCCCG	AGCCTGCTTG	GAGACCTCCT	AGAGGAGAGG	1380
CAGAGATAA	AGAAGAAGAT	GAAGGCCACG	ATTGACCCGA	TCGAGAGGAA	GCTCCTCGAT	1440
TACAGGCAGA	GGGCCATCAA	GATCCTGGCA	AACAGCTACT	ACGGTTACTA	CGGCTATGCA	1500
AGGGCGCGCT	GGTACTGCAA	GGAGTGTGCA	GAGAGCGTAA	CGGCCCTGGG	AAGGAGTAC	1560
ATAACGATGA	CCATCAAGGA	GATAGAGGAA	AAGTACGGCT	TTAAGGTAAT	CTACAGCGAC	1620
ACCGACGGAT	TTTTTGGCCAC	AATACCTGGA	GCCGATGCTG	AAACCGTCAA	AAAGAGGCT	1680
ATGGAGTTCC	TCAAGTATAT	CAACGCCAAA	CTTCCGGGCG	CGCTTGAGCT	CGAGTACGAG	1740
GGCTTCTACA	AACGGGCTTT	CTTCTGTCACG	AAGAAGAAGT	ATGCGGTGAT	AGACGAGGAA	1800
GGCAAGATAA	CAACGGCGGG	ACTTGAGATT	GTGAGGCGTG	ACTGGAGCGA	GATAGCGAAA	1860
GAGACGCAGG	CGAGGGTTCT	TGAAGCTTTG	CTAAAGGACG	GTGACGTCGA	GAAGGCCGTG	1920
AGGATAGTCA	AAGAAGTTAC	CGAAAAGCTG	AGCAAGTACG	AGGTTCCGCC	GGAGAAGCTG	1980
GTGATCCACG	AGCAGATAAC	GAGGGAATTA	AAGGACTACA	AGGCAACCGG	TCCCCACGTT	2040
GCCGTTGCCA	AGAGGTTGGC	CGCGAGAGGA	GTCAAAATAC	GCCCTGGAAC	GGTGATAAGC	2100
TACATCTGTG	TCAAGGGCTC	TGGGAGGATA	GCGCACAGGG	CGATACCGTT	CGACGAGTTC	2160
GACCCGACGA	AGCACAAGTA	CGACGCCGAG	TACTACATTG	AGAACCAAGT	TCTCCACGCC	2220
GTTGAGAGAA	TTCTGAGAGC	CTTCTGGTTAC	CGCAAGGAAG	ACCTGCGCTA	CCAGAAGACG	2280
AGACAGGTTG	GTTTGAGTGC	TTGGCTGAAG	CCGAAGGGAA	CT	2325	

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTA GTT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA TAT GAT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTT CCA TTT CCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA	

Replacement

Figure

Figure 17FF

(PCNA) - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC 54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA 108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC 216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA 270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA 324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA 378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT 432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT 486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT 540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA 594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
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ATGATCCTCG ACATGACTA CATAACCGAG GATGAAAGC CTGTCATAAG AATTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCTCGG GAGACCAGTT 240
GAGGTCCTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCCTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
```

Replacement

Figure

GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
 AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTTGGA AGAACGTGGA TCTCCCCTAC 540
 GTTGACGTGC TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
 AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGACAACT TCGACTTCGC CTATCTGAAA 660
 AAGCGTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
 ATTACAGAGG TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTTCGATCTC 780
 TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
 GCCGTCTTCG GTCAGCCGAA GGAGAAAGGTT TACGCTGAGG AAATAACCCAC AGCCTGGGAA 900
 ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
 GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCCAGCTTT CTGCTTTAAT CGGCCAGTCC 1020
 CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
 GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
 CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCCGAGA GAGGGTTGTG GGAGAACATA 1200
 GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
 GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
 CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
 AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCCTGGG AAGGGAGTAC 1560
 ATAAAGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
 ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGGC CGCTTGAGCT CGAGTACGAG 1740
 GGCTTCTACA AACCGGGCTT CTTCTGTACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
 GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
 GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTGCA GAAGGCCGTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
 GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCCG TCCCCACGTT 2040
 GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
 TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCAGCC 2220
 GTTGAGAGAA TTCTGAGAGC CTTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
 AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17GG

Replacement

Figure

(PCNA) -Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC      54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA      108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG      162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC      216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA      270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA      324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA      378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT      432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT      486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT      540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA      594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA      648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA      702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
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ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGCCGA GAGACATGGA 180
AAAACGTGTA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGT CCTTGCCCTT 420
GATATTGAAA CGTTTATCA TGAGGGAGAT GAATTTGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCAGATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
```

Replacement

Figure

CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGAAAA TCAAGGGTAG AATCCACTTT 780
 GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
 TATGAAGCAG TTTTtaggAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
 TGGGAAACAG AAGAAAGCAT GAAAAAActA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
 ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
 CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
 AGGGTGGCAT ACGCGAGGAA TGAACCTTGA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
 CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAAA AGGTTTGTGG 1200
 GAAAAATATCA TTTATTGTGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
 GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA 1320
 GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
 GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAAGAA 1440
 ATGCTCGATT ATAGGCAAAG GGCTATTAA TTTGCTTGCA ACAGCTATTA CGGCTATATG 1500
 GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTCTG AAAGCGTTAC CGCATGGGG 1560
 AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
 TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
 AAGAAAGCCA AGGAATTCCT AAAC TACATA AAC TCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
 GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
 GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
 ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACCTT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
 ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTTACTT 2160
 ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG TAG 2325

Figure 17HH

Vent DNA POLYMERASE - (PCNA) FUSION PROTEIN

Replacement

Figure

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 67)
 Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACCTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
 AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCTTCATT TTCAGCCCTA TATATATGCT 120
 CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
 AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
 GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
 AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
 CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGT CCTTGCCTTT 420
 GATATTGAAA CGTTTATCA TGAGGGGAGAT GAATTTGAA AGGGCGAGAT AATAATGATT 480
 AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACAATGGA AAAATATCGA TTTGCCGTAT 540
 GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
 AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCAT 660
 AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GCTTTAGGAA GGGACAAAGA ACATCCCGAA 720
 CCCAAGATTC AGAGGTGGG TGATAGTTTT GTCTGTGAAA TCAAGGTAG AATCCACTTT 780
 GATCTTTTCC CAGTTGTGCG AAGACGATA AACCTCCCA CGTATACGCT TGAGGCAGTT 840
 TATGAAGCAG TTTTLAGGAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
 TGGGAAACAG AAGAAAGCAT GAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
 ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
 CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
 AGGGTGGCAT ACGCGAGGAA TGAACCTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
 CGGCGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
 GAAAATATCA TTTATTGGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
 GTATCCCCAG ATACCCCTGA AAAAGAGGGC TGTAAAGAATT ACGATGTTGC TCCGATAGTA 1320
 GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTTATCCCT CCATACCTCGG GGACTTAATT 1380
 GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
 ATGCTCGATT ATAGGCAAG GGCTATTAAA TTGTTGCAA ACAGCTATTA CGGCTATATG 1500
 GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
 AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
 TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
 AAGAAAGCCA AGGAATTCCT AAACCTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
 GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800

Replacement

Figure

GATGAAGAGG	GCAGGATAAC	AACAAGGGGC	TTGGAAGTAG	TAAGGAGAGA	TTGGAGTGAG	1860
ATAGCTAAGG	AGACTCAGGC	AAAGGTTTTA	GAGGCTATAC	TTAAAGAGGG	AAGTGTGAA	1920
AAAGCTGTAG	AAGTTGTTAG	AGATGTTGTA	GAGAAAATAG	CAAAATACAG	GGTTCCACTT	1980
GAAAAGCTTG	TTATCCATGA	GCAGATTACC	AGGGATTTAA	AGGACTACAA	AGCCATTGGC	2040
CCTCATGTGC	CGATAGCAAA	AAGACTTGCC	GCAAGAGGGA	TAAAAGTGAA	ACCGGGCACA	2100
ATAATAAGCT	ATATCGTTCT	CAAAAGGGAG	GGAAAGATAA	GCATATAGGT	AAATTTTACTT	2160
ACAGAATACG	ATCCTAGAAA	ACACAAGTAC	GATCCGGACT	ACTACATAGA	AAACCAAAGTT	2220
TTGCCGGCAG	TACTTAGGAT	ACTCGAAGCG	TTTGGATACA	GAAAGGAGGA	TTTAAAGGTAT	2280
CAAAGCTCAA	AACAAACCGG	CTTAGATGCA	TGGCTCAAGA	GG 2325	//	
ATG CCA	TTT GAA	ATC GTA	TTT GAA	GGT GCA	AAA GAG	TTT GCC CAA CTT ATA GAC 54
ACC GCA	AGT AAG	TTA ATA	GAT GAT	GAG GCC	GCG TTT	AAA GAT GAA GAT GGG ATA 108
AGC ATG	AGG GCC	ATG GAT	CCA AGT	AGA GAT	GTT GTC	CTG ATT GAC CTA AAT CTC CCG 162
TCA AGC	ATA TTT	AGC AAA	TAT GAA	GTT GAT	GTT GAA	CCA ACA ATT GGA GTT AAC 216
ATG GAC	CAC CTA	AAG AAG	ATC CTA	AAG AGA	GGT AAA	GCA AAG GAC ACC TTA ATA 270
CTC AAG	AAA GGA	GAG GAA	AAC TTC	TTA GAG	ATA ACA	ATT CAA GGA ACT GCA ACA 324
AGA ACA	TTT AGA	GTT CCC	CTA ATA	GAT GTA	GAA GAG	ATG GAA GTT GAC CTC CCA 378
GAA CTT	CCA TTT	ACT GCA	AAG GTT	GTA GTT	CTT GGA	GAA GTC CTA AAA GAT GCT 432
GTT AAA	GAT GCC	TCT CTA	GTG AGT	GAC AGC	ATA AAA	TTT ATT GCC AGG GAA AAT 486
GAA TTT	ATA ATG	AAG GCA	GAG GGA	GAA ACC	CAG GAA	GTT GAG ATA AAG CTA ACT 540
CTT GAA	GAT GAG	GGA TTA	TTG GAC	ATC GAG	GTT CAA	GAG GAG ACA AAG AGC GCA 594
TAT GGA	GTC AGC	TAT CTC	TCC GAC	ATG GAT	GTT AAA	GGA CTT GGA AAG GCC GAT GAA 648
GTT ACA	ATA AAG	TTT GGA	AAT GAA	ATG CCC	ATG CAA	ATG GAG TAT TAC ATT AGA 702
GAT GAA	GGA AGA	CTT ACA	TTC CTA	CTG GCT	CCA AGA	GTT GAA GAG TGA

Figure 17II

Deep Vent- (PCNA) DNA polymerase fusion protein

Replacement

Figure

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG	ACGCTGACTA	CATCACCGAG	GATGGGAAGC	CGATTATAAG	GAITTTCAAG	60
AAAGAAACG	CGGAGTTTAA	GGTTGAGTAC	GACAGAAACT	TTAGACCTTA	CAITTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCTTGGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCT	CAGGACXXXC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTTCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGCCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGTCTGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAAG	720
ATGCAGAGTG	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCCTC	780
TACCACCTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAGCCCAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAGG	GACTGGAGAG	AGTTGCAAAG	TATTCATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCCG	AGAAAGGGGT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGTTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAACACAGT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTTGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACCTGGAG	GAAAAGTTCCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTCTGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAAGG	GGGACTGGAG	CGAAATAGCC	1860

Replacement

Figure

AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920			
GTAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980			
CTAGTTATTT	ACGAGCAGAT	CACGAGGCCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040			
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100			
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160			
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTACCT	2220			
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAAG	AAGACCTCAG	GTGGCAGAAG	2280			
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG //		2328			
ATG CCA	TTT GAA	ATC GTA	TTT GAA	GGT GCA	AAA GAG	TTT GCC	CAA CTT	ATA GAC	54
ACC GCA	AGT AAG	TTA ATA	GAT GAG	GCC GCG	TTT AAA	GTT ACA	GAA GAT	GGG ATA	108
AGC ATG	AGG GCC	ATG GAT	CCA AGT	AGA GAT	GTT GTC	CTG ATT	GAC CTA	AAT CTC	162
TCA AGC	ATA TTT	AGC AAA	TAT GAA	GTT GAT	GAA CCA	GAA ACA	ATT GGA	GTT AAC	216
ATG GAC	CAC CTA	AAG AAG	ATC CTA	AAG AGA	GGT AAA	GCA AAG	GAC ACC	TTA ATA	270
CTC AAG	AAA GGA	GAG GAA	AAC AAC	TTC TTA	GAG ATA	ACA ATT	CAA GGA	ACT GCA	324
AGA ACA	TTT AGA	GTT CCC	CTA ATA	GAT GTA	GAA GAG	ATG GAA	GTT GAC	CTC CCA	378
GAA CTT	CCA TTC	ACT GCA	AAG GTT	GTA GTT	CTT GGA	GAA GTC	CTA AAA	GAT GCT	432
GTT AAA	GAT GCC	TCT CTA	GTG AGT	GAC AGC	ATA AAA	TTT ATT	GCC AGG	GAA AAT	486
GAA TTT	ATA ATG	AAG GCA	GAG GGA	GAA ACC	CAG GAA	GTT GAG	ATA AAG	CTA ACT	540
CTT GAA	GAT GAG	GGA TTA	TTG GAC	ATC GAG	GTT CAA	GAG GAG	ACA AAG	AGC GCA	594
TAT GGA	GTC AGC	TAT CTC	TCC GAC	ATG GAT	GTT AAA	GGA CTT	GGA AAG	GCC GAT	648
GTT ACA	ATA AAG	TTT GGA	AAT GAA	ATG CCC	ATG CAA	ATG GAG	TAT TAC	ATT AGA	702
GAT GAA	GGA AGA	CTT ACA	TTC CTA	CTG GCT	CCA AGA	GTT GAA	GAG TGA		

Figure 17JJ

(PCNA) - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 38)

Replacement

Figure

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
GAT GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG	60
AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT	120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG	180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT	240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA	300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC	360
CTAATAGACA AAGGCCCTAAT TCCAAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT	420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA	480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC	540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG	600
AAAGATCCC ATGTATATAAT TACCTACAAC GGCAGTTCTT TCGACCTTCC CTATCTAGTT	660
AAGAGGCGG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG	720
ATGCAGAGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC	780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG	840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG	900
ACTGGAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAA GGTAAACGTAC	960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC	1020

Replacement

Figure

CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCA	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAAAGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGAGGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAAC'TGGAG	GAAAAGTTTCG	GGTTCAAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTTCGT	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGATAG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTAATT	ACGAGCAGAT	CACGAGGCCC	CTTACAGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CAITGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17KK

JDF-3 - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 67)

Replacement

Figure

GTT ACA ATA AAG TTTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA 702
 GAT GAA GGA AGA CTTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17LL

(PCNA) - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC	54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA	108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC ATT GAC CTA AAT CTC CCG	162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC	216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA	270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA	324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA	378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GGA GAA GTC CTA AAA GAT GCT	432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT	486
GAA TTT ATA ATG AAG GCA GAG GGA ACC CAG GAA GTT GAG ATA AAG CTA ACT	540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA	594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA	648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA	702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //	

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAGCCCGTCTATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAAGATTGAATACGACCGCGAGTTCGAGCC
 CTACTTCTACGCGTCCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGAGAGGACCGCAGGGTCTGTTAAGGTTAAGCGCGGAGAAAGGTGA
 AGAAAAAGTTCTCGGAGGTCTGTGGAGGTCTGGGTCTCTACTTCACGCACCCCGAGGACXXXCCGGCAATCCCGACAAAAATAAGGAAGCACCCCGCGGTCAATC
 GACATCTACGAGTACGACATACCCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTCTGAGATCGA
 JACGCTCTACCCAGGGAGAAAGAGTTTGGAAACCGGGCCGATTCTGTATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATAACCTGGAAGAAGATCGACCTTC

Replacement

Figure

CTTACGTTGAGGTGTCTCCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTCGTGATAACATACAACGGCGACAACCTTC
GACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAAGCTTGGCGTGAGCTTTTACCCCTCGGGAGGGACGGGAGCGAGCCGAAGATACAGCGCATGGGGGACAGGTTTTCGGGT
CGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCAATAAGGCGCACCATAAACCTCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGC
CCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCTTGGGAGACCGGCGAGGGCTTGAGAGGGTCCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAG
CTTGGCAGGGAGTTCTTCCGATGGAGGCCAGCTTTCCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCCT
CCTAAGGAAGGCCCTACGAGAGGAACGAACCTCGCTCCCAACAAGCCCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGCTACGcCGGTGGCTACGTCGAAGGAGCCGG
AGCGGGGACTGTGGGACAAATATCGTGTATCTAGACTTTTCGTAGTCTCTA[CC]TCAATCAATAATCACCCACAACGTCCTGCCAGATACGTCGAACCGCGAGGGGTGT
AGGAGCTACGACGTTGCCCCGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTTCATTCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAGATAAA
GAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAACTCTCTCGATTACAGGCAACG[CC]ATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATG
CCAGGGCAAGATGGTACTGCAAGGAGTGCGCCGAGCGTTACGGCATGGGGAAGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAGTTTCGGTTTAA
GTCCCTATGCAACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAACT
GCCCCGCCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAAGGGCTTCTTCGTCAAGAAAGAAAGTACGCGGTCAATCGACGAGGAGGCAAGATAACACGCGCG
GGCTTGAGATAGTCAGGCGCGACTGGAGCGGAGATAGCGAAGGAGACGCAAGGCGAGGTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAATT
GTCAGGGAAGTCAACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACCGCGAGCTCAAGGACTACAAGGCCACCGGCC
GCACGTAGCCATAGCGAAGCGTTTGGCCGCGAGAGGTGTTAAATCCGGCCCCGGAACCTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGG
CGATTCCCTTCGACGAGTTTCGACCCGACGAAGCAAAAGTACGATGCGGACTACTACATCGAGAACCAAGTTCTGCCGCGAGTTGAGAGAAATCTTCAGGGCCTTCGGGC
TACCGCAAGGAAGACCTGCGCTACCAAGAAGACGAGGCAGGTTCGGGCTTGGCGCGTGGCTGA

Replacement

Figure

Figure 17MM

Sac7d gene (ACCESSION No: M87569)

Nucleotide sequence (SEQ ID NO: 69)

Amino acid sequence (SEQ ID NO: 70)

```

M   V   K   K   V   K   K   F   K   Y   K   G   E   E   K   E   V   D   T   S      18
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA      54

K   I   K   K   V   W   R   V   G   K   M   V   S   F   T   Y   D   D      36
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC      108

N   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L      54
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA      162

L   D   M   L   A   R   A   E   R   E   K   K   *
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA TAA      67
                                         201
```

Figure 17NN

Sac7d-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 70) // Amino acid sequence (SEQ ID NO: 66)

```

M   V   K   K   V   K   F   K   K   Y   K   G   E   E   K   E   V   D   T   S
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA

K   I   K   K   V   W   R   V   G   K   M   V   S   F   T   Y   D   D
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC

N   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
```

Replacement Figure

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L D M L A R A E R E K K //
TTA GAC ATG TTA GCA AGA GAA GAG AAG AAA //

G G G
// GGC GGC GGT

V T S G M L P L F E P K G R V L L V
GTC ACT AGT GGG ATG CTG CCC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D G H H L A Y R T F H A L K G L T T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A V Y G F A K S L L K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V F D A K A P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L A R L E V P G Y E A D D V L A S L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K

```

Replacement Figure

GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG
 G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
 A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
 A H M D D L K L S W D L A K V R T D
 GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
 L P L E V D F A K R R E P D R E R L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
 R A F L E R L E F G S L L H E F G L
 AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
 L E S P K A L E E A P W P P E G A
 CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG CCG GAA GGG GCC
 F V G F V L S R K E P M W A D L L A
 TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
 L A A A R G G GGC GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
 CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
 A L R E G L G L P P G D D P M L L A
 GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
 Y L L D P S N T T P E G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
 G E W T E E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

Replacement Figure

A N L W G R L E G E E R L L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG

 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

 A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC GTC CTG GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC ACG GGC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

Replacement Figure

G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCG GCC AAG ACC ATC

 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

 K V R A W I E K T L E E G R R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG CGG GGG TAC

 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

 T A A D L M K L A M V K L F P R L E
 ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

 E M G A R M L L Q V H D E L V L E A
 GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

 P K E R A E A V A R L A K E V M E G
 CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

 V Y P L A V P L E V E V G I G E D W
 GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

 L S A K E G I D G R G G G G H H H
 CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC CAT CAT CAT

 H H *
 CAT CAT TAA

Replacement Figure

Figure 1700

Taq DNA polymerase- Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 69)

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 70)

```

      G   G   G
      // GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   V   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTC GGC AGC CTG

A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
```

Replacement Figure

D L Y Q L L S D R I H V L H P E G Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
GCC GAC TAC CCG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L K L S W D L A K V R T D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT

L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG CCG GAA GGG GCC

F V G F V L S R R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC

L A A A R G G R V H R A P E P Y K A
CTG GCC GCC AGG AGG GGC GGC CTG CAC CGG GCC CCC GAG CCT TAT AAA GCC

L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

Replacement Figure

Y L L D P S N T T P E G G V A R R Y G
 TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC

 G E W T E A G E R A A L S E R L F
 GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

 A N L W G R L E G E E R L L W L Y R
 GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG

 E V E R P L S A V L A H M E A T G V
 GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

 R L D V A Y L R A L S L E V A E E I
 CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

 A R L E A E V F R L A G H P F N L N
 GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

 S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GTC CTC GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A A F I A E E G W L L V A L D Y

Replacement Figure

ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT
 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC
 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC
 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC
 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC
 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC
 K V R A W I E K T L E E G R R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC
 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG
 K S V R E A A E R M A F N M P V Q G
 AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
 T A A D L M K L A M V K L F P R L E
 ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG
 E M G A R M L L Q V H D E L V L E A
 GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC
 P K E R A E A V A R L A K E V M E G
 CCA AAA GAG AGG GCG GAG GCC GTG GCC CTG GCC AAG GAG GTC ATG GAG GGG
 V Y P L A V P L E V E V G I G E D W
 GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

Replacement Figure

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaaatt
taagatagag catgatagaa ctttttagacc atacattttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg gaaaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaaagtctct cggaagcct attaccgtgt ggaaacttta
tttggaacat cccaagatg tcccactat tagagaaaaa gttagagaaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaacctcta
tcacgaagga gaagagttag gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaaagcaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaacctga
gagagtggcc aaataactga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaaccttg tagagtgggt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaga aggtcaggg agagctacac

Replacement Figure

aggtaggttc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccga ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaat ctttctacgg atattatggc tatgcaaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataaagag
gggattcttc gttacgaaga agaggtagtc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggctct cagtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
agggcatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct

Replacement Figure

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aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcaattcaa acgccttcgt tagaaatggt
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga ctctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct
acaatttttt ccttgatatct cctaattgat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt ttggaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataact gtctcaaatt atgacaaactc ttgacatttt tacttcatta
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnn nngtctctctc
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatggtgtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgtttagc tcntccenga
aagattgaga tgttcttgg //

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

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Replacement Figure

TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //TGA

Figure 17QQ

Sac7d - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 61)

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// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //
//
ccctggctct ggggtccacat atatgttctt actcgccctt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaaatt
taagatagag catgatagaa ctttttagacc atacattttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaggcat ggaagattg tgagaattgt
tgatgtagag aagggttga aaggtttct cggcaagcct attaccgtgt ggaacttta
tttggaaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaatagc atattccatt tgcaaaagaga tacctcatcg acaaggcct
aataccaatg gagggggaag aagagctaaa gattcttgcc ttogatatag aaacctcta
```

Replacement Figure

tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaagg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttctgac ttgtatcatg taataacaaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cttttatggg atgtttcaaag
gtcaagcaca gggaaaccttg tagagtgggt cttacttagg aaagcctacg aaagaaaacga
agtagctcca acaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac
aggtggattc gttaaagagc cagaaaaagg gtgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagtctt gcaaggacat
ccctggtttt ataccaagtc tcttgggaca ttgtttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaat ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg

Replacement Figure

gaaggagctc gaagaaaaagt ttggatttaa agtcctctac attgacactg atggctctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataaagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaattt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaaga ccattacatg agtataaggc gataggctct cacgtagctg ttgcaaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaaatggt
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt

Replacement Figure

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tttgctcaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct
acaatttttt ccttgatatc cctaattgat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataaact gtctcaaatt atgacaaactc ttgacatttt tacttcatta
ccagggtaat gttttttaagt atgaaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgtagc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaa taccagacga caatgggtg ctcactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga
aagattgaga tgttcttgg // TGA

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Figure 17RR

Sac7d - PFU DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 27)

Nucleotide sequence (SEQ ID NO: 69) //Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

Replacement Figure

ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

 ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
 AAAGAGAACG GAAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCATGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATT GGAACATCCC CAAGATXXXC CCACATTATT AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
 GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
 AAAAGGGCAG AAAAAGTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTGG GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGAGAGAA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAAGG 1140
 CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCGGATAC TC AATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAACTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA TAGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTG GGAAGAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAA TTTGTAATAA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCTGT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAAGCT 1920
 GTGAGAAATAG TAAAGAAAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAG 1980

Replacement Figure

CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGTCCCTCAC 2040
 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTTCCA 2220
 GCGGTACTTA GGATATTGGA GGAATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
 // TGA

Figure 17SS

PFU DNA POLYMERASE (V93 R OR E) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 69)
 Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
 AAAGAGAAG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
 CTTCTCAGG ATGATTCAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCG CAAGCCTATT 240
 ACCGTGTGGA AACTTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTTC 420
 GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
 GTTAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGAG 600
 AAGGATCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGACTTCCC ATATTAGCG 660
 AAAAGGGCAG AAAAATCTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCGAGGAA TAGGCGATAT GACGGCTGTA AAGTCAAGG GAAGATACA TTTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTTT GAAAGCCAAA GGAGAAAGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020

Replacement Figure

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TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTG GGAAGAAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TAGCATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCTTGGCTT AACATTAAAA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

```

Figure 17TT

PFU DNA POLYMERASE (G387P/V93R OR E) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69)

Replacement Figure

G387p Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAAGC GAAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGG ATGATTTCAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTTATT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAAATGA AGCAAAAGGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAAGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGTCCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAAG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTATG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATATC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAAG TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTTCT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCTCG GGGAAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAT TTGTAAAAATA CATAAATTC AAGTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGTTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAA TCATTACTCG TGGTTTTAGG ATAGTTGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAT TTTTGGAGACA ATACTAAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCCAAT ATGAAATTC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCTCTAC 2040

Replacement Figure

GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

Figure 17UU

PFU DNA POLYMERASE (G387P/V93R OR E) -Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69)
 Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
 V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAA 60
 AAAGAGAACG GAAAATTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
 CTTCTCAGGG ATGATTCAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTGTC AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420

GATATAGAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAATGA AGCAAAGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
 GTTAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTAGCG 660
 AAAAGGGCAG AAAAATTTGG GATTAATTTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAACTCAAGG GAAGAATACA TTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTTG GAAAGCCAAA GGAGNAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCACCTTAT 960
 GAACTCGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACT 1020
 TTATGGGATG TTTCAGAGTC AAGCACAGG AACCCTTGAG AGTGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAGG 1140
 CTCAGGGAGA GCTACACAGTTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAA 1200
 ATAGTATACC TAGATTTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
 CCGGATATC TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGNA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAATTTCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCGCTG GGGAGAGAA 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAGTTTG GATTTAAAGT CTTCTACAT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAAT TTGTAAAATA CATAAATTTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCCTTCGTT ACAGAGAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAAG TCATTTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAATC AAGCTAGAGT TTTGGAGACA ATACTAAAAAC ACGGAGATGT TGAAGAGGCT 1920
 GTGAGAAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTTCC ACCAGAGAA 1980
 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGGCGAT AGTCCCTCAC 2040
 GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAAAT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGAA 2160
 TACGATCCCA AAAGACAAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAA 2280
 ACAAGACAAG TCGGCCTAAC TTCTCTGGCTT AACATTAAAA AATCC // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

Replacement Figure

Figure 17VV

SAC7D-PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 31)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTTCAA GATTTGAAGAA GTTAAAGAAA TAACGGGGA AAGGCATGGA 180
AAGATTTGGA GAATTTGTTGA TGTAGAGNAG GTTGAGAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTTATTT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAA AGCTAAAGAT TCTTGCCCTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCG AGTAAAATGA AGCAAAGGTG ATTACTTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTTAGCG 660
AAAAGGGCAG AAAAACCTTG GATTTAAATTA ACCATTTGGA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAAGATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGA AAGAATTCCT TCCAATGGAA ATTCACTTTT CAAGATTAGT TGGACACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGG AACCTTTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAGGAAG 1140

Replacement Figure

CTCAGGGAGA GCTACACAGTTGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATT TAATTACCCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGACATTT GTTAGAGGAA 1380
 AGACAAAAAG TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGAC AAAAAAGCGAT AAAACTCTTA GCAAAATTTCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCCTG GGGAAAGAAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAAT TTGTAAATA CATAAATTCA AAGTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAAGAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAA 1980
 CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAAGCGAT AGGTCCTCAC 2040
 GTAGCTGTTG CAAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAAG 2280
 ACAAGACAAAG TCGGCCTAAC TTCTGGGCTT AACATTAAAA AATCC // 2328

TGA

Figure 17WW

KOD DNA POLYMERASE - Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATCCTCG ACACGTACTA CATAACCGAG GATGGAAGC CTGTATAAG AATTTTCAAG 60
 AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
 CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGG 180
 ACGGTTGTAA CGGTTAAGCG GGTGAAAAAG GTTCAGAAGA AGTTCTCGG GAGACCAGTT 240
 GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXIC CAGCGATAAG GGACAAGATA 300

Replacement Figure

CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGATATAGT GCCAATGGAA GGCACGAGG AGCTGAATAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGCCCAAT CTTATGATA 480
AGCTACGCCG ACCAGGAAGG GGCAGGGTG ATAACTTGA AGAACGTGA TCTCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGTG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCG ACCTTCTCAT AACCTACAC GGCACAACT TCGACTTCG CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCG AATAAACCTC GCCCTCGGA GGGATGGAAG CGAGCCGAAG 720
ATTGAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGTTGAGGC GGTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAAGTT TACGCTGAGG AAATAACAC AGCTGGGA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCGC TACTCGATGG AAGATGCGAA GGTACATAC 960
GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCAGCTTT CTGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
GCCATAGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGT GGCCAGAGA 1140
CGGCAGAGCT ATGAGGAGG CTATGTAAA GAGCCCCGAGA GAGGTTTGT GAGAGACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAAGATAA AGAAGAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCA GATCCTGGCA AACAGTACT ACGTTACTA CGGCTATGCA 1500
AGGGCGCGT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCTGGGG AAGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCGGGGC CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGA 1800
GGCAAGATAA CAACGCGCG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAA 1860
GAGACGCGAG CGAGGGTTCT TGAAGCTTTG CTAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGATTTA AAGGACTACA AGGCAACCGG TCCACCGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCTGTC TCAAGGCTC TGGGAGGATA GCGCAGAGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAATA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

Replacement Figure

Figure 17XX

Sac7d - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATCTCTG ACACCTGACTA CATAACCGAG GATGGAAGC CTGTCAATAAG AATTTTCAAG 60
AAGGAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCTTA CTCTACGCC 120
CTCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAGA TAACCGCGA GAGGCACGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAGA AGTTCCTCGG GAGACCAATT 240
GAGTCTGGA AACTTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCTTTCG CAAGCGCTAC 360
CTCATAGACA AGGATTTAGT GCCAATGGAA GCGACGAGG AGCTGAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCCGCC AGGGGCCAAT CCTTATGATA 480
AGCTACGCC ACGAGGAAGG GGCCAGGTG ATAACTTGA AGAACGTGA TCTCCCTAC 540
GTTGACGTC TCTCGACGGA GAGGAGATG ATAAAGCGT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCG ACGTTCTCAT AACCTACAAC GCGGACAAC TCGACTTCG CTATCTGAA 660
AAGCGCTGT AAAAGCTCG AATAAACTTC GCCCTCGGA GGGATGGAAG CGAGCCGAAG 720
ATTTCAGAGG TGGCGACAG GTTTGCCGTC GAAGTGAAG GACGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTT CCCACATACA CGTTGAGGC CGTTTATGAA 840
GCCGTCTCG GTCAGCCGAA GGAGAAGGT TACGCTGAG AAATAACCA AGCCTGGAA 900
ACCGGCGGA ACCTTGAGAG AGTCGCCGC TACTCGATGG AAGATCGGA GGTCACTAC 960
GAGCTTGGGA AGGAGTTCTT TCCGATGGAG GCCAGCTTT CTGCTTAAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGC AACCTCGTTG AGTGGTTCTT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAGCCCGAGA GAGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260

Replacement Figure

GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCAGG ATTTATCCCG AGCTGCTTG GAGACTCTCT AGAGAGAGG 1380
 CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTACTA CGGCTATGCA 1500
 AGGGCGCGT GGTACTGCAA GGAGTGTCA GAGAGCGTAA CGGCCTGGG AAGGAGTAC 1560
 ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
 ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
 GGCTTCTACA AACCGCGCTT CTTCTGTCACG AAGAAGAAGT ATCGGTGAT AGACGAGGAA 1800
 GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGCGTG ACTGGAGCGA GATAGCGAAA 1860
 GAGACGAGG CGAGGGTTCT TGAAGCTTGT CTAAGGACG GTGACGTGGA GAAGGCCGTG 1920
 AGGATAGTCA AGAAGTTAC CGAAAAGCTG AGCAAGTAC AGGTTCCGCC GGAGAAGCTG 1980
 GTGATCCACG AGCAGATAAC GAGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
 GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAATAC GCCCTGGAAC GGTGATAAGC 2100
 TACATCTGTC TCAAGGGCTC TGGGAGGATA GGCAGACGG CGATACCGTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCGGT TCTCCAGCC 2220
 GTTGAGAGAA TTCTGAGAGC CTTGCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
 AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17YY

Sac7d-Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

ATGATACTGG ACACGTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAG 60
 AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCTCATTT TTCAGCCCTA TATATATGCT 120
 CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180

Replacement Figure

AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTACAGGAAAA AATTTTGGG AAGGGAAGTT 240
 GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXKXC CAGCTATGCG GGGCAAAATA 300
 AGGGAACATC CAGCTGTGGT TGACATTTTAC GAATATGACA TACCCCTTGC CAAGCGTTAT 360
 CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
 GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
 AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
 GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAAGT TGTAAAGAA 600
 AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCAT 660
 AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
 CCCAAGATTG AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
 GATCTTTTCC CAGTTGTGCG AAGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
 TATGAAGCAG TTTTAGGAAA AACCAAAAGC AATTAGGAG CAGAGGAAAT TGCCGCTATA 900
 TGGAAACAG AAGAAAGCAT GAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
 ACGTATGAGC TCGGGAAGGA ATTCCTTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
 CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
 AGGGTGGCAT ACGCGAGGAA TGAACCTTGA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
 CGGCGCTTAA GAACAACCTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
 GAAAATATCA TTTATTGTGA TTTCCGCGAT CTGTACCCTT CAATAATAGT TACTCACAA 1260
 GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAAAT ACGATGTTGC TCCGATAGTA 1320
 GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACCTCG GGACTTAATT 1380
 GCAATGAGGC AAGATATAAA GAAGAAATG AAATCCACAA TTGACCCCGAT CGAAAAGAAA 1440
 ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTTGCAA ACAGCTATTA CGGCTATATG 1500
 GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
 AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCCGGCT TAAGGTTCTT 1620
 TATCGGGACA CTGACGGCTT TTAATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
 AAGAAAGCCA AGGAATTCTT AAACCTACATA AACCTCAAAC TTCCAGGTCT GCTTGAGCTT 1740
 GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTTACAA AAAAGCGCTA TGCAGTCA 1800
 GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
 ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACCTT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAGTGAA ACCGGGCACA 2100
 ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
 ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 17ZZ

Vent DNA POLYMERASE - Sac7d FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACAC TGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTGAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAAATTGGAA AGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAAG GGCAGAGTA ATCAGATGGA AAAATATCGA TTGCGCGTAT 540
GTGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
CCCAAGATTG AGAGGATGGG TGATAGTTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAAGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGTGGCAT ACGCGAGGAA TGAAC TTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGGCTTAA GAACAACCTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTTATTTGGA TTTCCGCAGT CTGTACCCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCCTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTTATCCCT CCATACCTCGG GGACTTAAAT 1380

Replacement Figure

```

GCAATGAGGC AAGATATATAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTA 1680
AAGAAAGCCA AGGAATTCCT AAACCTACATA AACTCCAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGG AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACCTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA // TGA

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Figure 17AAA

Deep Vent- Sac7d DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 69)

Replacement Figure

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACCTTG	ACGCTGACTA	CATCACCGAG	GATGGGAAGC	CGATTATAAG	GATTTCAAG	60
AAAGAAAAACG	CCGAGTTTAA	GGTTGAGTAC	GACAGAAACT	TTAGACCTTA	CATTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCTCTGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCCT	CAGGACXXIC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATTT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCGTTCCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	TCCAATGGAA	GGCGATGAAG	AGCTCAAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAAGT	GATAAAGGAG	600
AAAGATCCCG	ATGTTTATAAT	TACCTACAA	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720
ATGCAGAGGC	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAAGCCAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGAAAAGG	GACTGGAGAG	AGTTGCAAAG	TATTCAATGG	AGGATGCAAA	GGTAAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAAGCTT	CAAGGTTAGT	CGGCCAGGCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAAATGAAT	GGTCCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAAG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAAGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCA	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAAGCT	TCTAAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGAGGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACTGGAG	GAAAAGTTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAAATTCCT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAAGAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCACG	GGCTGTTGGA	GCCTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTTCGTG	ACGAAGAAGA	AGTATGCCGT	GATAGATGAG	1800
GAAGGGAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAAACC	AAGCAAAAAT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACCT	TGAGGAGGCA	1920
GTAAGAGATAG	TTAAGGAGGT	AACGTGAAAAG	CTGAGCAAGT	ACGAATATACC	TCCAGAAAAAG	1980
CTAGTTTATTT	ACGAGCAGAT	CACGAGGCC	CTTTCACGAGT	ACAAAGGCTAT	AGGTCCGCAC	2040
GTTGCCCGTG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160

Replacement Figure

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TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

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Figure 17BBB

Sac7d - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 37)
 Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
 AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
 AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
 TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
 AAAGAAAACG GCGAGTTTAA GGTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT 120
 CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
 AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCTCTGG GAGGCCGATT 240
 GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
 AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC 360
 CTAATAGACA AAGGCCTAAT TCCAATGGAA GCGGATGAAG AGTCAAGTT GCTCGCATTT 420
 GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCCA AGGGGCCCAT TATAATGATA 480
 AGCTATGCTG ATTAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
 GTCGAGGTAG TTTCCAGCGA GAGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
 AAAGATCCCG ATGTTATAAT TACCTACAAC GCGGATTTCTT TCGACCTTCC CTATCTAGTT 660
 AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAAG 720
 ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
 TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG 840
 GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG 900
 ACTGGAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC 960
 GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
 CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
 GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
 CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG 1200
 TTAGTTTCCC TAGATTTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
 CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTGGGCAC 1320

Replacement Figure

AAGTTCGTGA	AGGACTTCCC	GGGGTTTATC	CCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACCTGGAG	GAAAAGTTTCG	GGTTCAAAGT	CTTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCCCT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAAGAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	ACGTGAGAGG	GTTCTTCTGT	ACGAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAAGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGAGTAG	TTAAGGAGGT	AAC TGAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTTACA	TAGAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAAG TAA		2328

Figure 17CCC

JDF-3 - Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 69)

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAGCCCGTCAATCAGGGTCTTCAAGAGAGAAACGGCGAGTTCAGGATTGAATACGACCGGAGTTCGAGCCCTACTTCT
ACGGCTCCTCAGGAGCAGCTCTGCCATCGAAGAAATCAAAAGATACCGCGGAGAGGACGGCAGGGTCTGTTAAGTTAAGCGCGGAGAGAGGTGAAGAAAAAGTTTCTCGG
CAGGTCTGTGGAGTCTGGTCTCTTACTTTCACGCACCCCGGAGGACXXXCCGGCAATCCGGACAAAATAAGGAAGCACCCCGGTCATCGACATCTACGAGTACGACATACCC
TTCCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAACTCATGTCTCTTGGAGACGCTCTACCGAGGAGAGGTTGGAA
CCGGCCGATTTCTGATGATAAGCTACGCCGATGAAGCGAGGGCGCGTGATAACCTTGAAGAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAA
GCGCTTCTTGGGGTCTGTTAAGGAGAAGGACCCGGACGTCTGTATAACATACACGGCGACAACTTTCGACTTTCGCCTACCTGAAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTT
ACCTTCGGGAGGACGGAGCGGAGCCGAAGATACAGCGCATGGGGACAGGTTTTCGGTCGAGGTGAAGGGCAGGTTACACTTCGACCTTTATCCAGTCAATAAGGCGCACCATAA
ACCTCCCGACCTACACCTTTGAGGCTGTATACGAGGCGGTTTTTCGGCAAGCCCAAGGAGAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGCGGAGGGCTTGAGAG

GGTCGGCGCTACTCGATGGAGGACGCGAGGGTTACTACGAGCTTGGCAGGGAGTTCTTCCGATGGAGGCCAGCTTTCCAGGCTCATCGGCCAAGGCCCTCTGTGGACGTTTCCCGCTCAGACCGGCCAACCTCGTCGATGGTTCCTCTTAAGGAAGCCTACGAGAGAACGAACTCGCTCCCAACAAGCCCGACGAGAGGAGCTGGCGAGGAGAAAGGGGGGGCTACGCGGTGGCTACGTCGAAGGAGCCGGAGCGGGGACTGTGGACAATATCGTGTATCTAGACTTTCTAGTCTCTACCTTCAATCATATATCACCCACAACGCTCTCGCCAGATACGCTCAACCCGCGAGGGGTGTAGGAGCTACGACGTTGCCCGGAGGTCGCAAGTCTGCAAGGACTTCCCGGCTCATTCGAGCTGCTCGGAAACCTGCTCGGAGGAAAGGCAGAGAATAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAACTCTCTCGATTACAGGCAACGGCCATCAAGAATTCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCAGGGCAAGATGGTACTCGAGGGAGTGC CGGAGCGTTACGGCATGGGAAGGGAGTACATCGAAATGGTTCATCAGAGAGCTTGAGGAAAAAGTTCCGTTTTTAAAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTTCTTGAGCGGACGCTGAAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACATATATCAATCCCAAATCGCCCGCTTCTGAACTCGAATACGAGGGCTTCTACGTCAGGGCTTCTTCTGTCAGGAAGAAAGTACGCGGTCTATCGAGAGGGCAAGATAACACCGCCGGCTTGAGATCTGAGTCAAGCGGACTGAGCAAGGAGACGCGAGGGTTTTTGAGGGCGATATCTAGGCACGGTGTAGAGGCGGTGAGAAATGTTCAGGGAATCAACCGAAAAAGCTGAGCAAATAAGAGGTTCCGCGGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCAGTAGCCATAGCGAAAGCGTTTGGCCCGCCAGAGGTGTAAAAATCCGGCCCGGAACGTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGCGACAGGGCGATTCCCTTCGACGAGTTCCGCCGACGAGCAAGATACGATGCGGACTACTACATCGAGAACGAGGTTCTGCCGGCAGTTGAGAGAACTCTCGGCTACCGAAGACGAGGACGAGGTTCGGGCTTGGCGCTGAGGCTGAGGCTGAGGCTTCTTCCGATGGAGGCCAGCTTTCCAGGCTCATCGGCCAAGGCCCTCTCGAGGCTCTGTGGACGTTTCC

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TAG

Figure 17DDD

Sac7d - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTG GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

Replacement Figure

//ATGATCCTTGAGTTGATTACATACCGAGAATGGAAGAAGCCCGTCATCAGGGTCTTCAAGAAGAGAAACGGCGAGTTCAGGATTGAATACGACCGGAGTTTCGAGGCCCTACTT
CTACCGCGCTCCTCAGGGACGACTCTGCGCATCGAAGAAATCAAAAAGATAAACCGCGGAGAGGCACGGCAGGGTCGTTAAGTTAAGCGCGGAGAGAGGTGAAGAAAAAAGTTTCCTC
GGCAGGTCTGTGGAGGTCTGGGTCTCTACTTTCACCGCACCCGAGGACXXXCXCGCAATCCCGGACAAAAATAAGGAAGCACCCCGGTATCGACATCTACGAGTACGACATAC
CCTTCGCCAAAGCGCTACCTCATAGACAAGGGCTTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTC[GAG]ATCGAGACGCTCTACCCAGGAGGAGAGAGTTTGG
AACCGGGCCGATTCTGATGATAAGCTACCGCGATGAAAGCGGCGCGGTGATAAACCCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAAAGGAGATGATT
AAGCGCTTCTTGAGGGTCGTTAAGGAGAGAGCCCGGACGTGCTGATAACATAACAACGGCGACAACTTTCGACTTCGCCCTACCTGAAAAAAGCGCTGTGAGAAGCTTTGGCGTGAGCT
TTAACCTCGSGAGGGACGGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTGGCGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCAATAAGGCGCACCAT
AAACCTCCCGACCTACACCTTTGAGGCTGTATACGAGGGCGGTTTTTCGGCAAGCCCAAGGAGAAAGGTCTACGGCGAGGAGATAGCCACCGCTGGGAGACCAGGAGGGGCTTGAG
AGGGTCGCGCGCTACTCTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTT
CCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCTCTTAAGGAAGGCCCTACGAGAGGAACGAAACTCGCTCCCAACAGGCCCGACGAGAGGAGCTGGCGGAGGAGAAAGGGGGG
CTACGcCGGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGGACAAATATCGTGTATCTAGACTTTTCGTAGTCTCTA[CC]TTCATCATAATCAACCAACGTCCTCGCCAGAT
ACGCTCAACCCGCGAGGGGTGTAGGAGCTACGACGTTTGCCCGAGGTCCGTGCAAGAACTTCTCGATTACAGGCAACG[GC]ATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGG
GGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAAGAACTCTCGCATGGGGAAGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAAGTTTCGGTTTAAAGTC
CTATGCCAGGGCAAGATGGTACTGTGAGGGAGTGGCCGAGAGCGTTACGGCATGGGGAAGGAGTACATCGAAATGGCAATGGAGTTCTTAAACTATATCAATCCCAAACCTGCCCGGCTTC
CTCTATGCAACACAGACGGTCTCCATGCCACCAATTCCTGGAGCGGACGCTGAACAAGTCAAGAAACAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACCTGCCCGGCTTC
TCGAACTCGAATAAGAGGGCTTCTACGTACGGGGCTTCTTCGTACGAAAGAAAGTACGCGGTCTATCGACGAGGGCAAGATAACCAACGCGCGGGCTTGAGATAGTACAGGCG
CGACTGGAGCGAGATAGCGAAGGAGACGCGAGGCGGATACTCAGGCACGGTGACGTTTGGAGCGGATACTCAGGCAAGGTGAGAGGCGGTGAGAAAGTTCAGGGGAAGTCAACGAAAAAGCTGAGC
AAGTACGAGGTTCCGCGCGGAGAGCTGTGTTATCCACGAGCGAGATAACGCGCGGAGCTCAAGGCTACAGGCCACCGGCCAGTACGCAAGCGTAAGCGAAGCGTTTGGCCCGCAGAG
GTGTTAAAAATCCGGCCCGGAACCTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGGCGACAGGGCGATTCCCTTCGACGAGTTTCGACCGAGTTCGACCGAAGCAAGTACGA
TGCGGACTACTACATCGAGAACCAGGTTCTCGCGGCTACCGCAAGGAAGACCTCGGCTACCGAAGAGACGAGGCAAGGTCGGGCTTGGC
GCGTGGCTGAAGCCGAAGGGGAAGAAGTGA

Figure 17EEE

Synthetic Sso7d gene:

Nucleotide sequence (SEQ ID NO: 71)

Amino acid sequence (SEQ ID NO: 72)

```
A  T  V  K  F  K  Y  K  G  E  E  K  E  V  D  I  S  K
GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

I  K  K  V  W  R  V  G  K  M  I  S  F  T  Y  D  E  G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

G  G  K  T  G  R  G  A  V  S  E  K  D  A  P  K  E  L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

L  Q  M  L  E  K  Q  K  K
CTG CAG ATG CTG GAG AAG CAG AAA AAG
```

Figure 17FFF

Sso7d-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 65)

Amino acid sequence (SEQ ID NO: 72) // Amino acid sequence (SEQ ID NO: 66)

```
// A  T  V  K  F  K  Y  K  G  E  E  K  E  V  D  I  S  K
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

I  K  K  V  W  R  V  G  K  M  I  S  F  T  Y  D  E  G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

G  G  K  T  G  R  G  A  V  S  E  K  D  A  P  K  E  L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

L  Q  M  L  E  K  Q  K  K  //  G  G  G
CTG CAG ATG CTG GAG AAG CAG AAA AAG //  GGC GGC GGT
```

Replacement Figure

V T S G M L P L F E P K G R V L L V
 GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTC GTG

D G H L A Y R T F H A L K G L T T
 GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S R G E P V Q A V Y G F A K S L L K
 AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

A L K E D G D A V I V F D A K A P
 GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

S F R H E A Y G G Y K A G R A P T P
 TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E D F P R Q L A L I K E L V D L L G
 GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTC GGG

L A R L E V P G Y E A D D V L A S L
 CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTC GTG GCC AGC CTG

A K K A E K E G Y E V R I L T A D K
 GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

D L Y Q L L S D R I H V L H P E G Y
 GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L I T P A W L W E K Y G L R P D Q W
 CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A D Y R A L T G D E S D N L P G V K
 GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G I G E K T A R K L L E E W G S L E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A L L K N L D R L K P A I R E K I L
 GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A H M D D L L K L S W D L A K V R T D

GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC
L P L E V D F A K R R E P D R E R L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT
R A F L E R L E F G S L L H E F G L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CTC CAC GAG TTC GGC CTT
L E S P K A L E E A P W P P E G A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC
F V G F V L S R K E P M W A D L L A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT CTG GCC
L A A A R G G R V H R A P E P Y K A
CTG GCC GCC AGG GGC GGC GGC CTC CAC CGG GCC CCC GAG CCT TAT AAA GCC
L R D L K E A R G L L A K D L S V L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG
A L R E G L G L P P G D D P M L L A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC
Y L L D P S N T T P E G V A R R Y G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC
G E W T E E A G E R A A L S E R L F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC
A N L W G R L E G E E R L L W L Y R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG AGG CTC CTT TGG CTT TAC CGG
E V E R P L S A V L A H M E A T G V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTC GGC CAC ATG GAG GCC ACG GGG GTG
R L D V A Y L R A L S L E V A E E I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC
A R L E A E V F R L A G H P F N L N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC CAC CCC TTC AAC CTC AAC

S R D Q L E R V L F D E L G L P A I
 TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

 G K T E K T G K R S T S A A V L E A
 GGC AAG ACG AAG ACC GGC AAG CGC TCC ACC AGC GCC GGC CTC CTG GAG GCC

 L R E A H P I V E K I L Q Y R E L T
 CTC CGC GAG GCC CAC CTC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

 K L K S T Y I D P L P D L I H P R T
 AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

 G R L H T R F N Q T A T A T G R L S
 GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GCC AGG CTA AGT

 S S D P N L Q N I P V R T P L G Q R
 AGC TCC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG CTT GGG CAG AGG

 I R R A F I A E E G W L L V A L D Y
 ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

 S Q I E L R V L A H L S G D E N L I
 AGC CAG ATA GAG CTC AGG GTG CTC GGC CAC CTC TCC GGC GAC GAG AAC CTG ATC

 R V F Q E G R D I H T E T A S W M F
 CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

 G V P R E A V D P L M R R A A K T I
 GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCC AAG ACC ATC

 N F G V L Y G M S A H R L S Q E L A
 AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

 I P Y E E A Q A F I E R Y F Q S F P
 ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

 K V R A W I E K T L E E G R R R G Y
 AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

 V E T L F G R R R Y V P D L E A R V
 GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

Replacement Figure

```

K S V R E A A E R M A F N M P V Q G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

T A A D L M K L A M V K L F P R L E
ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E M G A R M L L Q V H D E L V L E A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

P K E R A E A V A R L A K E V M E G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V Y P L A V P L E V E V G I G E D W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

L S A K E G I D G R G G G G G G H H H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGC CAT CAT CAT CAT

H H *
CAT CAT TAA

```

Figure 17GGG

Pfu DNA Polymerase (WT) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 71)

```

//
cccttggtcct ggggtccacat atatgtttctt actcgcccttt atgaagaatc ccccgatcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat
caactctaca cctccccctat tttctctctt atgagatttt taagtatatg tatagagaag
gtttttact ccaaaactgag ttagtagata tgtgggggagc ataattgatt tagatgtgga

```

Replacement Figure

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaaatt
 taagatagag catgatagaa ctttttagacc atacattttac gctcttctca gggatgattc
 aaagattgaa gaagttaaga aaataacggg gaaaaggcat ggaaagattg tgagaattgt
 tgatgtagag aaggttgaga aaagtttct cggcaagcct attaccgtgt ggaaacttta
 tttggaacat cccaagatg ttccactat tagagaaaaa gtagagaaac atccagcagt
 tgtggacatc ttcgaatacg atattccatt tgcaaaagaga tacctcatcg acaaaggcct
 aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaacctcta
 tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
 tgaagcaaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
 cgagagagag atgataaaga gatttctcag gattatcagg gagaaaggatc ctgacattat
 agttacttat aatggagact cattcgactt cccatattta gcgaaaaaggg cagaaaaaact
 tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
 tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
 gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
 aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga
 gagagttgcc aaataactga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
 ccttccaatg gaaattcagc tttcaagatt agttggacaa cttttatggg atgtttcaag
 gtcaagcaca gggaaaccttg tagagtgggt ctacttagg aaagcctacg aaagaaacga
 agtagctcca aacaagccaa gtgaagagga gtatcaaga aggctcaggg agagctacac
 aggtggattc gttaaagagc cagaaaaaggg gttgtgggaa aacatagtat acctagattt
 tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct

Replacement Figure

tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
 ccctggtttt ataccaagtc tcttgggaca ttgttttagag gaaagacaaa agattaagac
 aaaaatgaag gaaactcaag atcctataga aaaaatactc cttagactata gacaaaaagc
 gataaaactc ttagcaaaatt ctttctacgg atattatggc tatgcaaaaag caagatggta
 ctgtaaggag tgtgtcgaga gcgttactgc ctgggggaaga aagtacatcg agttagtatg
 gaaggagctc gaagaaaaagt ttggattttaa agtcctctac attgacactg atggtctcta
 tgcaactatc ccaggaggag aaagtgagga aataaaagaaa aaggctctag aatttgtataa
 atacataaat tcaaaagctcc ctggactgct agagcttgaa tatgaagggt ttataaagag
 gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
 tcgtggttta gagatagtta ggagagattg gagtgaattt gcaaaaagaaa ctcaagctag
 agtttttgag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
 agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
 gataacaaga ccattacatg agtataaggc gataggctct cactagctg ttgcaaaagaa
 actagctgct aaaggagtta aaataaaagcc aggaatggta attggataca tagtacttag
 aggcgatggg ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaaagca
 caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtag ttaggatatt
 ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
 aacttctctg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
 tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
 tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc

Replacement Figure

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tttgctaagt gaatagaata aacaacatca ctcaattcaa acgccttcgt tagaaatggt
ctatctgcat gcttctcttg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctcaa gcagagccgc tccaatggat aacacccctg ttccccgacc caagtccgct
acaatttttt ccttgatatct cctaattgtat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataaact gtctcaaatt atgacaaactc ttgacatttt tacttcatta
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc
ctcgatttcc ttggttgctgc tccatatgat aagcttccaa agtgggtgtt cagactttta
gacactcaaa taccagacga caatggtgtg ctcaactcaag ccccatatgg gttgagaaaa
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnaga
aagattgaga tgttcttg //
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

```

Figure 17HHH

PFU DNA POLYMERASE (V93 R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTTT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCCTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTAGCG 660
AAAAGGCAG AAAAAGCTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAAACAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGT GAAAGCCAAA AGTGGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAAGT AAGAGGAGTA TCAAGAAGAG 1140
CTCAGGGAGA GCTACACAGG TGGATTCTGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTATG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGACATTTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680

Replacement Figure

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GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAAATC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2280
ACAAACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC 2328
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

```

Figure 17III

PFU DNA POLYMERASE (G387P/V93R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 71)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```

ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACATTATT AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTTCC ATATTAGCG 660
AAAAGGGCAG AAAAATCTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720

```

Replacement Figure

ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCTT TCCAATGGAA ATTCAAGCTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCTGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATATCT TAAATCTTGA GGGATGCAAG AACTATGATA TCGTCTCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA TAGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCGCTG GGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAGACCA TTACATGAGT ATAAGCGGAT AGTCCCTCAC 2040
GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Figure 17JJJ

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 71)

Replacement Figure

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTATG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTTCAA GATTGAAGAA GTTAAAGAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTTATT GGAACATCCC CAAGATXXXC CCACATATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCCTGCCCTTC 420
GCNATAGCNA CCTCTATCA CGAAGGAGAA GAGTTTGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCT ATATTTAGCG 660
AAAAGGCGAG AAAAATCTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAG GAAGAATACA TTTTCGACTTG 780
TATCATGTAA TAAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTGT GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGTCCAAAAC AAGCCAAAGT AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA GTTGGATTCTGT AAAGAGCCAG AAAAGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTATG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAGAA 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCCTATGTC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
AAAGGAAAAG CACTTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTTGCA 1860
AAAGAACTC AACTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCCTAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTCTTCCCA 2220

Replacement Figure

GCGGTACTTA GGATATTGGA GGGATTGTGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCTGGCTT AACATTAAAA AATCC // 2328
 // GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Figure 17KKK

KOD DNA POLYMERASE - Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 71)
 Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 ATGATCCTCG ACATGACTA CATAACCGAG GATGAAAGC CTGTACATAAG AATTTTCAAG 60
 AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTCTACGCC 120
 CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
 ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCTCGG GAGACCAGTT 240
 GAGGTCGTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
 CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
 CTCATAGACA AGGGATTAGT GCCAATGGAA GCGGACGAGG AGCTGAAAAT GCTCGCCTTC 420
 GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTGCGCG AGGGGCCAAT CCTTATGATA 480
 AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACGTGA TCTCCCTAC 540
 GTTGACGTG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
 AAAGACCCCG ACGTTCTCAT AACCTACAAC GCGGACAAC TCGACTTCGC CTATCTGAAA 660
 AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
 ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
 TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGTTGAGGC CGTTTATGAA 840
 GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCA AGCCTGGGAA 900
 ACCGGCGAGA ACCTTAGAG AGTCGCCCG TACTCGATGG AAGATCGGAA GGTCAACATAC 960
 GAGTCTGGGA AGGATTTCTT TCCGATGGAG GCCGACTTTT CTGCTTTAAT CGGCCAGTCC 1020
 CTCTGGGAG TCTCCCGTTC CAGCACTGGC AACCTCGTTG AGTGGTTTCTT CCTCAGGAAG 1080
 GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
 CGGCAGAGCT ATGAAGGAGG CTATGTAAA GAGCCCCGAG GAGGGTTGTG GGAGAACATA 1200
 GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
 GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380

Replacement Figure

CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGTACTT ACGTTACTA CGGCTATGCA 1500
 AGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCTGGGG AAGGAGTAC 1560
 ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
 ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
 GGCTTCTACA AACCGGCTT CTTGCTCAG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
 GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
 GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAGGACG GTGACGTCGA GAAGGCCGTG 1920
 AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGTTCCGCC GGAGAAGCTG 1980
 GTGATCCAG AGCAGATAAC GAGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
 GCCGTGCCA AGAGGTTGGC CGCGAGGATA GGCACAGGG CGATACCGTT CGACGAGTTC 2100
 TACATGTCG TCAAGGGTC TGGGAGGTA GCGACAGGG TACTACATTG AGAACCAGGT TCTCCCAGCC 2160
 GACCCGACG AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
 GTTGAGAGAA TTTCGAGAGC CTTGCGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
 AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325

 // GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Figure 17LLL

Sso7d - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 33)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG //

Replacement Figure

//ATGATCCTCG ACACTGACTA CATAACCGAG GATGAAAGC CTGTACATAAG AATTTTCAAG 60
 AAGGAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCCTA CTTTACGCC 120
 CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGCACGGG 180
 ACGGTTGTAA CGGTTAAGCG GGTGAAAAG GTTCAGAAGA AGTTCTCTCG GAGCCAGTT 240
 GAGGCTGGGA AACTCTACTT TACTCATCCG CAGGACXXC CAGCGATAAG GGACAAGATA 300
 CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
 CTCATAGACA AGGGATTAGT GCCAATGGAA GCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
 GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCC AGGGCCCAAT CCTTATGATA 480
 AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGA AGAACGTGA TCTCCCTTAC 540
 GTTGACGTG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
 AAAGACCCGG ACGTTCTCAT AACCTACAAC GCGACAACCT TCGACTTCGC CTATCTGAAA 660
 AAGCGTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
 ATTACAGAGA TGGGCGACAG GTTTGCCGTC GAAGTGAAG GACGGATACA CTTGATCTC 780
 TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGTTGAGGC CGTTTATGAA 840
 GCCGTCTCG GTACGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCCAG AGCCTGGGAA 900
 ACCGGCGAGA ACCTTGAGAG AGTCGCCCG TACTCGATGG AAGATGCGAA GGTACACATAC 960
 GAGCTTGGGA AGGAGTTTCT TCCGATGGG GCCCAGCTTT CTGCTTAAAT CGGCCAGTCC 1020
 CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGTTTCTT CCTCAGGAAG 1080
 GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
 CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCCGAGA GAGGTTGTG GGAGAACATA 1200
 GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
 GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCACAGGT CGGCCACCGC 1320
 TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCTGTCTG GAGACCTCCT AGAGGAGAGG 1380
 CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
 TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGTTTACTA CGGCTATGCA 1500
 AGGGCGCGCT GGTACTGCAA GGAGTGTGA GAGAGCGTAA CGGCTGGGG AAGGGAGTAC 1560
 ATAACGATGA CCATCAAGGA GATAGAGGA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
 ACCGACGGAT TTTTGTCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
 ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
 GGCTTCTACA AACCGGCTT CTTCTGCACG AAGAAGNAGT ATCGGTGAT AGACGAGGAA 1800
 GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
 GAGACGACAG CGAGGTTTCT TGAAGCTTTG CTAAGGACG GTGACGTCGA GAAGCCGTG 1920
 AGGATGTCA AAGAAGTTAC CGAAAAGCTG AAGGAAGTAC AGGTTCCGCC GGAGAAGCTG 1980
 GTGATCCACG ACAGATAAC GAGGATTTA AAGCACTACA AGGCAACCGG TCCCCACGTT 2040
 GCCGTTGCCA AGAGTTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
 TACATCGTGC TCAAGGGCTC TGGGAGGATA GCGACACAGG CGATACCGTT CGACGAGTTC 2160
 GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACAGGT TCTCCAGCC 2220
 GTTGAGAGAA TTCTGAGAGC CTTGCTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
 AGACAGGTTG GTTTGAGTGC TTGCTGAAG CCGAAGGGAA CT //TAG 2325

Figure 17MMM

Sso7d-Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 35)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //

ATGATACTGG ACACGTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACGTGTA GAGTGTCTGA TGCAGTGAAG GTCAGGAAAA AATTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATTGGAG GGAGACGAGG AGCTTAAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCAGATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGCTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTTCTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACCTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAAATATCA TTTATTTTGA TTTCCGCAGT CTGTACCCCTT CAATAATAGT TACTCACAA 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATCCCTT CCATCTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAAATG AAATCCACAA TTGACCCCGAT CGAAAAAGAA 1440

Replacement Figure

ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
 GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
 AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
 TATCGGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
 AAGAAAGCCA AGGAATTCTT AAACCTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
 GAGTATGAGG GCTTTTACTT GAGAGGATTC TTGTGTACAA AAAAGCGCTA TGCAGTCATA 1800
 GATGAAGAGG GCAGGATAAC AACRAAGGGG TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
 ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAGAGAGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAATAG CAAAATACAG GGTCCACTT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTG CGATAGCAAA AAGACTTGCC GCAAGAGGA TAAAGTGAA ACCGGGCACA 2100
 ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTTACTT 2160
 ACAGAAATCG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTGTGGATACA GAAAGGAGGA TTTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325

Figure 17NNN

Vent DNA POLYMERASE - Sso7d FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTGG ACACTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTAAAG 60
 AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
 CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
 AAAAAGTGA GAGTGTCTGA TGCAGTGAAA GTACAGGAAA AATTTTGGG AAGGGAAGTT 240
 GAAGTCTGGA AGTCAATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
 AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
 CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAAGT CCTTGCCTTT 420
 GATATTGAAA CGTTTTATCA TGAGGGGAGAT GAAATTGGAA AGGGCGAGAT AATAATGATT 480
 AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCAGATGGA AAAATATCGA TTTTGCCGTAT 540
 GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTAAAGAA 600
 AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
 AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAAG ACATCCCGAA 720
 CCCAAGATTC AGAGGATGGG TGATAGTTT GCTGTGAAA TCAAGGGTAG AATCCACTTT 780
 GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840

Replacement Figure

TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
 TGGGAAACAG AAGAAAGCAT GAAAAAATA GCCCAGTACT CAATGGAAGA TGCTAGGCA 960
 ACGTATGAGC TCGGGAAGGA ATTCTTCCC ATGGAAGCTG AGCTGGCAA GCTGATAGGT 1020
 CAAAGTGAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
 AGGTGGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
 CGGCGCTTAA GAACAACCTA CCTGGGAGGA TATGTAAAG AGCCAGAAA AGGTTTGTGG 1200
 GAAAATATCA TTTTATTGGA TTTCCGCAGT CTGTACCCCTT CAATAATAGT TACTCACAAC 1260
 GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
 GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACCTCG GGACTTAATT 1380
 GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
 ATGCTCGATT ATAGGCAAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
 GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGG 1560
 AGACCTACA TAGAGTGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGTTCTT 1620
 TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGG AAAAGCCTGA ACTCATTTAA 1680
 AAGAAAGCCA AGGAATTCTT AAACATACATA AACTCCAAAC TTCCAGGCTT GCTTGAGCTT 1740
 GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
 GATGAAGAGG GCAGGATAAC AACAAAGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
 ATAGCTAAGG AGACTCAGG AAAGGTTTTA GAGGCTATAC TTTAAAGAGG AAGTGTGAA 1920
 AAAGCTGTAG AAGTTGTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCACCTT 1980
 GAAAAGCTTG TTATCCATGA GCAGATTACC AGGATTTAA AGGACTACAA AGCCATTGGC 2040
 CCTCATGTGC CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
 ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAGATAA GCGATAGGGT AATTTTACTT 2160
 ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
 TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTTAAGGTAT 2280
 CAAAGCTCAA AACAAACCG CTTAGATGCA TGGCTCAAGA GG 2325 //

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Figure 17000

Deep Vent- Ssod7 DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 71)

Replacement Figure

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG	ACGCTGACTA	CATCACCGAG	GATGGGAAGC	CGATTATAAG	GATTTTCAAG	60
AAAGAAAACG	GGGAGTTTAA	GGTTGAGTAC	GACAGAAACT	TTAGACCTTA	CAITTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	GATTGATGAG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	TGCCGAAAAG	GTAAGGAAGA	AGTTCTCTGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	TGAACACCCCT	CAGGACXXXC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	TGACATCTTT	GAGTACGACA	TTCCCGTTCCG	GAAGAGGTAC	360
CTAATAGACA	AAGGCCCTAAT	TCCNAATGAA	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	CGAAGGGGAG	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCCAAAGTC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTCCAGGTAG	TTTCCAGCGA	GAGGGAGATG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	600
AAAGATCCCG	ATGTATATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	660
AAGAGGGCCG	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCCAAAG	720
ATGCAGAGCG	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCAGG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAGAG	GACTGGAGAG	AGTTGCAAAAG	TATTTCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCA	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAAACAGT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAACCTGGAG	GAAAAGTTTCG	GGTTCAAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAAATTCCT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT	AGTCACTAGG	GTTCTTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCAGTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAAACC	AAGCAAAAAGT	CCTAGAGGCT	ATCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGATATG	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTTCATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAAATCA	GGTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAAG		2328

Replacement Figure

```
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA
```

Figure 17PPP

Ssod7 - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 37)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG //
```

```
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG 60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTACGCT 120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG 180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT 240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA 300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTTCG GAAGAGGTAC 360
CTAATAGACA AAGGCCATAAT TCCAATGGA GGCGATGAAG AGCTCAAGTT GCTCGCATTT 420
GACATAGAAA CCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA 480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC 540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG 600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCAGATTCTT TCGACCTTCC CTATCTAGTT 660
AAGAGGCCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG 720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC 780
```

Replacement Figure

TACCACGTGA	TTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
GCAATCTTCG	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
ACTGGAAGG	GACTGGAGAG	AGTTGCAAG	TAITCAATGG	AGGATGCAAA	GGTAACGTAC	960
GAGCTCGGTA	GGGAGTTCTT	CCCAATGGAG	GCCCAAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
CTGTGGGATG	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
GCCTACGAGA	GGAATGAATT	GGTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
CTAAGGGAGA	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
TTAGTTTCCC	TAGATTTTCA	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGTCTCA	1260
CCGGATACGC	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
AAGTTCTGCA	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAAGGAGTG	GCAGAGAGCG	TTACGGCCTG	GGGAGGGAA	1560
TATATAGAGT	TCGTAAGGAA	GGAAC TTGAG	GAAAAGTTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	CACAATTCTT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCTAGAGT	TCGTAGATTA	TATAAACGCC	AAGTCCCG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGTTCT	ACGTGAGAGG	GTTCTTCGTG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAAGGAAGA	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAGATAG	TTAAGGAGGT	AAC TGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT	ACGAGCAGAT	CACGAGGCC	CTTCACGAGT	ACAAGGCTAT	AGGTC CGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17QQQ

JDF-3 - Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)

V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAAATGAAAAGCCCGTCATCAGGGTCTTCAAGAAAGGAGAACGGCGAGTTCAGGATTGAAATACGACCGGAGTTCGAGCCCTACTTCT
ACGGCTCCTCAGGGACGACTGTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGGAGAGAGGTGAAGAAAAAGTTCCCTCGG
CAGGTCGTGGAGGTCGTGGTCTCTACTCTACGCACCGCCGAGGACXXXCCGGCAATCCGGACAAAATAAGGAAGCACCCCGCGGTCTACGACATCTACGAGTACGACATACCC

Replacement Figure

TTTCGCCAAGCGTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTCTTCGACATCGAGACGCTCTACCAAGAGGAGAAAGAGTTTGGAA
 CCGGGCCGATTCTGATGATAAGCTACGCCGATGAAGAGCGAGCGCGGTGATAACCTGGAAGAAGATCGACCTCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAA
 GCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGTGATAACATACACGGCGACAATTCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAGCTTTGGCGTGAGCTTT
 ACCCTCGGAGGACCGGAGCGGAGCCGAAGATACAGCGCATGGGGACAGGTTTGGCGTCAAGGAGAGTACCTTCGACCTTTATCCAGTCAATAAGGCGCACCATAA
 ACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGTCTACCGCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGGCTTGAGAG
 GGTCCGCGCTACTCGATGGAGGACCGGAGGTTTACCTACGAGCTTGGCAGGAGTTCCTCCCGATGGAGGCCAGCTTCCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCC
 CGCTCCAGCACCCGCAACCTCGTCGAGTGTTCCTCTTAAGGAGGCTACGAGAGGAACGAATCGCTCCCAACAAGCCGACGAGAGGAGCTGGCGAGGAGAAGGGGGGCT
 ACgCGGTGGCTACGTCAAGGACCGGAGCGGGGACTGTGGACAATATCGTGTATCTAGACTTTCGTAAGGACTTCCCGGCTTCATTCGAGGCTGCTCGGAAACCTGCTGGAGGAAAGG
 GCTCAACCCGCGAGGGGTGAGGAGCTACGACGTTGCCCGAGGTCGATCAAGTTCGCAAGGACTTCCCGGCTTCATTCGAGGCTGCTCGGAAACCTGCTGGAGGAAAGG
 CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAAATCTCCTCGATTACAGGCAACGGCGGATCAAGAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
 ATGCCAGGGCAAGATGGTACTGCAAGGAGTGC CGGAGAGCGTTACGGCATGGGAAGGAGTACATCGAAATGGTCAATCAGAGAGCTTGAGGAAAAAGTTTCGGTTTAAAGTCTCT
 CTATGCAGACACAGACCGTCTCCATGCCACCAATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCTTCTC
 GAACTCGAATACGAGGGCTTCTACGTCAGGGCTTCTTCGTACGAAGAAAAGTACGCGGTCTATCGACGAGGAGGCAAGATAACCAACGCGCGGGCTTGAGATAGTCAGGCGCG
 ACTGGAGCGAGATAGCGAAGGAGACGCGAGGAGGTTTGGAGCGGATCTCAGGCACGGTGTGAGAGGCCGTAGATTGTCAAGGAAAGTCAACGAAAAAGCTGAGCAA
 GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACCGCGAGCTCAAGGACTACAGGCCACCGGCCCGCATAGCGAAAGcGTTTGGCCCGCAGAGGT
 GTTAAATCCGGCCCGGAACTGTGATAAGCTACATCGTCTGAAAGGCTCCGGAAGGATAGGCGACAGGGGATTCCTTCGACGAGTTTCGACCCGACGAAGCAAGTACGATG
 CGGACTACTACATCGAGAACCAAGGTTCTGCCGCGAGTTGAGAGAATCTCAGGGCTTCGCGTACCCGAAGGAAGACCTCGGCTACCAAGAAGACGAGGCGAGGTTCGGGCTTGGCGC
 GTGGCTGAAGCCGAAGGGGAAGAAG//

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG // TAG

Figure 17RRR

Sso7d - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 39)

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGinine)
 V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
 ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
 GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG GAG CTG
 CTG CAG ATG CTG GAG AAG CAG AAA AAG //

Replacement Figure

ATGATCCTTGACGTTGATTACATCACCGAGAAATGGAAGAGCCCGTTCATCAGGGTCTTCAAGAAAGGAGAACCGCGAGTTTGAATATACGACCGCGAGTTTCGAGCCCTACTTCT
ACGGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGAGAGGACCGCAGGGTCGTTAAGTTAAGCGCGGAGAAAGGTGAAGAAAAAGTTCTCTCGG
CAGGTCTGTGGAGGTCTGGTCTCTACTTCACGCAACCGCAGGACXXXXCGGCAATCCGCGACAAATAAGGAAGCAACCCCGGGTTCATCGACATCTACGAGTACGACATACCC
TTCCGCAAGCGCTACCTCATAGACAAGGGCTTAATCCCGATGGAAGGTGAGAAAGAGCTTAAACTCATGTCTCTTGGATCGAGACGCTCTACCGAGGAGAAAGAGTTTGGAA
CCGGCCGATTTCTGATGATAAGCTACGCCGATGAAGCGAGGCGCGGTGATAAACCCTGGAAGAAGATCGACCTTCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAA
GCGCTTCTTGAGGTCGTTAAGGAGAGGACCCGACGTGCTGATAACATAACAACGGCGACAACCTTCGACTTCGCCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTT
ACCTTCGGGAGGACCGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTGGGTGAGGTGAAGGCGAGGTACACTTCGACCTTCCGCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTT
ACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGCTTGAGAG
GGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTTACCTACGAGCTTGGCAGGGAGTTTCTCCGATGGAGGCCAGCTTTCAGGCTCATCGGCCAAGGCCCTCTGGGACGTTTCC
CGCTCCAGCACCCGGCAACCTCGTCGAGTGGTTCTCTTAAGGAAGGCCCTACGAGAGGAACGAACCTCGTCCCAACCAAGCCCGACGAGAGGAGCTGGCGAGGAAGAGGGGGCT
ACGCGCGGTGGCTACGTCGAAGGAGCCGGAGCGGGGACTGTGGACAAATATCGTGTATCTAGACTTTTCGTAGTCTCTAqCCTTCAATCATAATCACCCACAACTGTCTCGCCAGATAC
GCTCAACCCGAGGGGTGTAGGAGCTACGACGTTTCCCCGAGGTCCGTCAAGTTCTGCAAGGACTTCCCCGGCTTCATTCAGAGCTGTCTCGGAAACCTGTGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAAATCTCTCGATTACAGGCAACCGqGCCATCAAGATTCTCGCCAAACAGCTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGGTACTGCAAGGAGTGCGCCGAGAGCGTTACGGCATGGGAAAGGAGTACATCGAAATGGTTCATCAGAGAGCTTGAGGAAAAAGTTTCGGTTTAAAGTCTCT
CTATGCAGACACAGACGGTCTCCATGCCACCAATCTCTGGAGCGGACCGTGAACAAGTCAAGAAAAAGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCTTCTC
GAATCGAATAACGAGGGCTTCTAAGTCAAGGGCTTCTTCGTCAAGAAAGAAAGTACGCGGTCTATCGACGAGGAGGCAAGATAACCAACCGCGGGCTTGAGATAGTACAGGCGG
ACTGGAGCGGATAGCGAAGGAGACGCAAGGCGAGGGTTTGGAGGCGGATACTCAGGCAAGGTGACGTTGAAGAGCGCTCAGAAATTGTCAAGGAAAGTCAACCGAAAAAGCTGAGCAA
GTACGAGGTTCCGCGGAGAAAGCTGGTTATCCAAGAGCAGATAACGCGGAGCTCAAGGCTACCAAGGCCACCGGCGGCAAGTAGCCATAGCGAAAGcGTTTGGCCCGCAGAGGT
GTTAAAAATCCGCGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTTCGACCCGACGAAGCAAGTACGATG
CGGACTACTACATCGAGAACCAGGTTCTGCGGCGAGTTGAGAGAATCCTCAGGGCTTTCGGCTACCGCAAGGAAGACCTGCGCTACCAAGAAGACGAGGCAAGTTCGGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAAGTGA

SEQ. ID. NOS.

a

MkTpV 1 valvydaefvgserfeeeeetfllkGtkaadov R 177 Rg KudeElielhq 73
Reca VI Gdnakkeyavvr drrlgaakkgdevvg 74

MkTpV 179 vpidk GILQ IL wtpbEAEAGLSVSeVgGkdpeessgiyslwsrvvvv 75
HTH asnC IDAfi ILGEL RRIS EAEAGLSVStVleVr 76

HTH SS α α

b

← Motif 1 → ← Motif 2 →

	299	354	411	468	518	568	622	696	752	803	855	912	EcRuvA	73	HsPolB	57	TaqPol	93	Consensus	HhH	SS
A	lk	at	ae	lk	ip	kf	wk	yk	lr	et	ka	ke	ke	ae	le	uu	gvg	A	ll	ygs	u
B	drY	deh	kke	si	re	nie	ler	rd	vnk	qvr	dvk	ktn	ktp	ae	klp	evp	gvg	A	ll	ygs	u
C	edv	alc	pda	ade	rta	ae	egr	rr	pae	er	ve	ka	dr	la	la	ae	pk	ta	rg	u	α
D	ra	eh	rk	rk	rk	er	ea	ey	kr	rr	er	ee	sg	ef	ea	ea	ll	ygs	u	α	α
E	sis	la	per	ysk	asa	lke	die	age	vsk	vs	wt	pyr	qqf	gkl	ds	u	α	α	α	α	α
F	iat	tpv	tlk	la	re	gve	rr	syd	np	eva	tpd	rk	pvs	lt	eks	na	er	ddt	s	u	α
G	la	tdl	elz	la	re	gve	rr	syd	np	eva	tpd	rk	pvs	lt	eks	na	er	ddt	s	u	α
H	la	tdl	elz	la	re	gve	rr	syd	np	eva	tpd	rk	pvs	lt	eks	na	er	ddt	s	u	α
I	la	tdl	elz	la	re	gve	rr	syd	np	eva	tpd	rk	pvs	lt	eks	na	er	ddt	s	u	α
J	la	tdl	elz	la	re	gve	rr	syd	np	eva	tpd	rk	pvs	lt	eks	na	er	ddt	s	u	α
K	la	tdl	elz	la	re	gve	rr	syd	np	eva	tpd	rk	pvs	lt	eks	na	er	ddt	s	u	α
L	la	tdl	elz	la	re	gve	rr	syd	np	eva	tpd	rk	pvs	lt	eks	na	er	ddt	s	u	α
EcRuvA	la	tdl	elz	la	re	gve	rr	syd	np	eva	tpd	rk	pvs	lt	eks	na	er	ddt	s	u	α
HsPolB	la	tdl	elz	la	re	gve	rr	syd	np	eva	tpd	rk	pvs	lt	eks	na	er	ddt	s	u	α
TaqPol	la	tdl	elz	la	re	gve	rr	syd	np	eva	tpd	rk	pvs	lt	eks	na	er	ddt	s	u	α
Consensus	la	tdl	elz	la	re	gve	rr	syd	np	eva	tpd	rk	pvs	lt	eks	na	er	ddt	s	u	α
HhH	la	tdl	elz	la	re	gve	rr	syd	np	eva	tpd	rk	pvs	lt	eks	na	er	ddt	s	u	α
SS	la	tdl	elz	la	re	gve	rr	syd	np	eva	tpd	rk	pvs	lt	eks	na	er	ddt	s	u	α

77/78 79/80/81 82 83/84/85 86/87/88 89/90/91 92/93 94/95 96/97/98 99/100/101 102/103/104 105/106/107 108/109 110 111/112/113

FIGURE 18 (cited from Belova et al. (2001) Proc. Natl. Acad. Sci 98: 6015-6020)

Replacement Figure

FIGURE 19

SEQ ID NO: 120 Synthetic Sso7d gene

GCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGACATCTCCAA
GATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTACGACGAGGG
CGGTGGCAAGACCGGCCGTGGTGCAGTAAGCGAAAAGGACGCGCCGAAGGAGC
TGCTGCAGATGCTGGAGAAG CAGAAAAAG

SEQ ID NO: 121 The amino acid sequence of Sso7d.

ATVKFKYKGEEKEVDISKIKKVWRVGMISFTYDEGGGKTGRGAVSEKDAPKELLQ
MLEKQKK

SEQ ID NO: 122 The DNA sequence encoding the Sso7d-ΔTaq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA
GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCAGTAAGCGAAAAG
GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG
TGTCAGTAGTCCCAAGGCGCTGGAGGAGGCCCCCTGGCCCCCGCCGAAGGGGGC
TTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCCTGTGGGCCGATCTTCTGGCCCT
GGCCGCCGCCAGGGGGGGCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCT
CAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGC
CCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTAC
CTCCTGGACCCTTCCAACACCAACCCCGAGGGGGTGGCCCGGCGCTACGGCGGG
GAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTCCGAGAGGCTCTTCGCC
AACCTGTGGGGGAGGCTTGAAGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAG
GTGGAGAGGCCCCCTTCCGCTGTCTGGCCACATGGAGGCCACGGGGGTGCGC
CTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCC
GCCTCGAGGCCGAGGTCTTCCGCTGGCCGGCCACCCCTTCAACCTCAACTCCC
GGACCAGCTGGAAGGGTCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAA
GACGGAGAAGACGGCAAGCGCTCCACGAGCGCCGCTCTGGAGGCCCTCCG
CGAGGCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTACCAAGCT
GAAGAGCACCTACATTGACCCCTTGCCGACCTCATCCACCCAGGACGGGCCG
CCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTC
CGATCCCAACCTCCAGAACATCCCGCTCCGCACCCCGCTTGGGCAGAGGATCCGC
CGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAG
ATAGAGCTCAGGGTGTGGCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCT
TCCAGGAGGGGCGGGACATCCACGAGACCGCCAGCTGGATGTTCCGGCTCC
CCCGGGAGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCG
GGGTCTCTACGGCATGTCGGCCACCGCCTCTCCAGGAGCTAGCCATCCCTTA
CGAGGAGGCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGG
GCCTGGATTGAGAAGACCTGGAGGAGGGCAGGAGGCGGGGTACGTGGAGAC
CCTCTTCGGCCGCCCGCTACGTGCCAGACCTAGAGGCCCGGTGAAGAGCGT
GCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCG
CGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGG
GGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCAAAAGA
GAGGGCGGAGGCCGTGGCCCGGTGGCCAAGGAGGTCATGGAGGGGGTGTATCC
CCTGGCCGTGCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGC
CAAGGAGGGCATTGATGGCCGCGCGGAGGCGGGCATCATCATCATCATTA A

SEQ ID NO: 123 The amino acid sequence of Sso7d-ΔTaq fusion protein

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGVTSKALEEAPWPPPEGAFFVGFVLSRKEPMWADLLALAA

ARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDP
SNTTPEGVARRYGGEWTEEAGERAAALSERLFANLWGRLEGEERLLWLYREVERPLS
AVLAHMEATGVRDLVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERVLF
DELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLIH
PRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDYS
QIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGV
LYGMSAHLRSQELAIPLYEEAQAFIERYFQSFPKVRWIEKTLEEGRRRGYVETLFGRR
RYVPDLEARVKSUREAAERMAFNMPVQGTAAADLMKLAMVKLFPRL EEMGARMLL
QVHDELVLEAPKERA EAVARLAKEVM EGVYPLAVPLEVEVGIGEDWLSAKEGIDGR
GGGGHHHHHH

SEQ ID NO: 124 The DNA sequence encoding the Sso7d-Taq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA
GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAAG
GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG
TGCTACTAGTGGGATGCTGCCCCTCTTTGAGCCCAAGGGCCGGGTCTCTCTGGTG
GACGGCCACCACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCA
GCCGGGGGGAGCCGGTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCTCAAGG
CCCTCAAGGAGGACGGGGACGCGGTGATCGTGGTCTTTGACGCCAAGGCCCCCT
CCTTCCGCCACGAGGCCTACGGGGGGTACAAGGCGGGCCGGGCCCCACGCCAG
AGGACTTTCCCCGGCAACTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCT
GGCGCGCTCGAGGTCCCGGGCTACGAGGCGGACGACGTCTGGCCAGCCTGGC
CAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCCTCACCGCCGACAAAG
ACCTTTACCAGTCTCTTTCCGACCGCATCCACGTCTCCACCCCGAGGGGTACCT
CATCACCCCGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCCGACCAGTGGGC
CGACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGG
CATCGGGGAGAAGACGGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAG
CCCTCCTCAAGAACCTGGACCGGTGAAGCCCGCCATCCGGGAGAAGATCCTGG
CCCACATGGACGATCTGAAGCTCTCTCTGGGACCTGGCCAAGGTGCGCACCGACCT
GCCCCTGGAGGTGGA CTTCGCCAAAAGGCGGGAGCCCGACCGGGAGAGGCTTAG
GGCCTTTCTGGAGAGGCTTGAGTTTGGCAGCCTCCTCCACGAGTTCGGCCTTCTG
GAAAGCCCCAAGGCGCTGGAGGAGGCCCCCTGGCCCCCGCCGAAGGGGCCTTC
GTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCTGG
CCGCCGCCAGGGGGGGCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCTCA
GGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCCC
TGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCTACCT
CCTGGACCCTTCCAACACCACCCCGAGGGGGTGGCCCCGGCGCTACGGCGGGGA
GTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTCCGAGAGGCTCTTCGCCAA
CCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAGGT
GGAGAGGCCCCCTTCCGCTGTCTTGCCACATGGAGGCCACGGGGGTGCGCCT
GGACGTGGCCTATCTCAGGGCCTTGTCCTTGAGGTGGCCGAGGAGATCGCCCG
CCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGG
GACCAGCTGGAAAGGGTCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAAG
ACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCGTCTGGAGGCCCTCCGC
GAGGCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTACCAAAGCTG
AAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCAGGACGGGCGGCC
TCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTCCG
ATCCCAACCTCCAGA. ACATCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCG
GGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGAT
AGAGCTCAGGGTGCTGGCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTC
CAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTCCGGCGTCCCC
CGGGAGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCGGG
GTCCTCTACGGCATGTGCGCCACCGCCTCTCCAGGAGCTAGCCATCCCTTACG
AGGAGGCCACGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGGGC

CTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGACCC
TCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGTGC
GGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGCCG
ACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGG
CCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGAGA
GGGCGGAGGCCGTGGCCCCGGCTGGCCAAGGAGGTGATGGAGGGGGTGTATCCCC
TGGCCGTGCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGCCA
AGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATTAA

SEQ ID NO: 125 The amino acid sequence of Sso7d-Taq fusion protein.

MITNSSATVKFKYGEEKEVDISKIKKVWRVGMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGSVTSGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGE
PVQAVYGFAKSLKALKEDGDAVIVVFDKAPSFRHEAYGGYKAGRPTPEDFPRQ
LALIKELVDLLGLARLEVPGYEADDVLASLAKKAEKEGYEVRLTADKDLYQLSDR
IHVLHPEGYLITPAWLWEKYGLR. PDQWADYRALTGDESDNLPVKGIGEKTARKLL
EEWGSLEALLKNLDRPKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREP
DRERLRAFLELLEFGSLLEHFGLESKALEEAPWPPPEGAFVGVLSRKEPMWADL
LALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLA
YLLDPSNTTPEGVARRYGGEWTEEAGERALSERLFANLWGRLEGEERLLWLYREV
ERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQL
ERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPL
PDLIHPRGTGRHLTRFNQTATATGRLSSSDPNLQNPVRTPLGQIRJRRAFIAEEGWLLVA
LDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTI
NFGVLYGMSAHRLSQELAIPEYEEAQAFIERFYQSFVKVRAWIEKTLEEGRRRGYVETL
FGRRRYVPDLEARVKSUREAERMAFNMPVQGTAAADLMKLAAMVKLFPRLEEMGA
RMLLQVHDELVEAPKERAEAVARLAKEVMGVPYPLAVPLEVEVGIGEDWLSAKE
GIDGRGGGGHHHHHH

SEQ ID NO: 126 The DNA sequence encoding the Pfu-Sso7d fusion protein

ATGATTTTATAGATGTGGATTACATAACTGAAGAAGGAAAACCTGTTATTAGGCTAT
TCAAAAAAGAGAACGGAATAATTAAGATAGAGCATGATAGAACTTTTAGACCAT
ACATTTACGCTCTTCTCAGGGATGATTCAAAGATTGAAGAAGTTAAGAAAATAAC
GGGGGAAAGGCATGGAAAGATTGTGAGAATTGTTGATGTAGAGAAGGTTGAGAA
AAAGTTTCTCGGCAAGCCTATTACCGTGTGGAACTTTATTTGGAACATCCCCAA
GATGTTCCCACTATTAGAGAAAAAGTTAGAGAACATCCAGCAGTTGTGGACATCT
TCGAATACGATATTCCATTTGCAAAGAGATACCTCATCGACAAAGGCCTAATACC
AATGGAGGGGGAAGAAGAGCTAAAGATTCTTGCCTTCGATATAGAAACCCTCTA
TCACGAAGGAGAAGAGTTTGAAAAGGCCCAATTATAATGATTAGTTATGCAGA
TGAAAATGAAGCAAAGGTGATTACTTGAAAAACATAGATCTTCCATACGTTGA
GGTTGTATCAAGCGAGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGA
GAAGGATCCTGACATTATAGTTACTTATAATGGAGACTCATTGACTTCCCATAT
TTAGCGAAAAGGGCAGAAAACTTGGGATTAAATTAACCATTGGAAGAGATGGA
AGCGAGCCCAAGATGCAGAGAATAGGCGATATGACGGCTGTAGAAGTCAAGGG
AAGAATACATTTGCACTTGTATCATGTAATAACAAGGACAATAAATCTCCCAACA
TACACACTAGAGGCTGTATATGAAGCAATTTTTGGAAAGCCAAAGGAGAAGGTA
TACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTT
GCCAAATACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTC
CTTCCAATGGAAATTCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTT
CAAGGTCAAGCACAGGGAACCTTGTAGAGTGGTTCTTACTTAGGAAAGCCTACG
AAAGAAACGAAGTAGCTCCAAACAAGCCAAGTGAAGAGGAGTATCAAAGAAGG
CTCAGGGAGAGCTACACAGGTGGATTCTGTTAAAGAGCCAGAAAAGGGGTTGTGG
GAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGATTATAATTACCC
ACAATGTTTCTCCCGATACTCTAAATCTTGAGGGATGCAAGAACTATGATATCGC
TCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTC

TTGGGACATTTGTTAGAGGAAAGACAAAAGATTAAGACAAAAATGAAGGAAACT
TTAGCAAATTCCTTTCTACGGATATTATGGCTATGCAAAAGCAAGATGGTACTGTA
AGGAGTGTGCTGAGAGCGTTACTGCCTGGGGAAAGAAAGTACATCGAGTTAGTAT
GGAAGGAGCTCGAAGAAAAGTTTGGATTTAAAGTCCTCTACATTGACACTGATG
GTCTCTATGCAACTATCCCAGGAGGAGAAAGTGAGGAAATAAAGAAAAAGGCTC
TAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCTTGAATA
TGAAGGGTTTTATAAGAGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAAT
AGATGAAGAAGGAAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTG
GAGTGAATTTGCAAAAGAACTCAAGCTAGAGTTTTGGAGACAATACTAAAAACA
CGGAGATGTTGAAGAAGCTGTGAGAATAGTAAAAGAAGTAATACAAAAGCTTGC
CAATTATGAAATTCACCAGAGAAGCTCGCAATATATGAGCAGATAACAAGACC
ATTACATGAGTATAAGGCGATAGGTCTCACGTAGCTGTTGCAAAGAACTAGCT
GCTAAAGGAGTTAAAATAAAGCCAGGAATGGTAATTGGATACATAGTACTTAGA
GGCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATCCCCAA
AAGCACAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCCAGCGGTA
CTTAGGATATTGGAGGGATTTGGATACAGAAAGGAAGACCTCAGATACCAAAAG
ACAAGACAAGTCGGCCTAACTTCCTGGCTTAACATTAATAAATCCGGTACCGGC
GGTGGCGGTGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGA
CATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTAC
GACGAGGGCGGTGGCAAGACCGGCCGTGGTGCAGTAAGCGAAAAGGACGCGCC
GAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGTGA

SEQ ID NO: 127 The amino acid sequence of the Pfu-Sso7d fusion protein

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERH
GKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFA
KRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIIMISYADENEAKVITWKND
LPYEVVSSSEREMIKRFLRIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS
EPKMQRIGDMTAAVEVKGRIFDLHYHVTIRTNLPTYTLEAVYEAIFGPKPEKVYADEI
AKAWESGENTLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGGPLWDVSRSTGN
LVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESYTGGFVKEPEKGLWENIVYLD
ALYPSIIITHNVSPDTLNLGCKNYDIAPQVGHKFC KDIPGFPSLLGHLLEERQKIKTK
MKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIE
LVWKELEEFKFKVLYIDTDGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYE
GFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDWSEIAKETQARVLETILKHGDVEE
AVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVKIKPG
MVIGYIVLRGDPISNRILAEEDPKKHKYDAEYYIENQVLPVLRILEGFGYRKED
LRYQKTRQVGLTSLWLNKSGTGGGGATVKFKYKGEEKEVDISKIKKVWRVGMIS
FTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

SEQ ID NO: 128 The DNA sequence encoding the Sac7d-ΔTaq fusion protein

atgattacga	attcgacggt	gaaggtaaag	ttcaagtata	aggggtgaaga	gaaagaagta
gacacttcaa	agataaagaa	ggtttgagaga	gtaggcaaaa	tggtgtcctt	tacctatgac
gacaatggta	agacaggtag	aggagctgta	agcgagaaaag	atgctccaaa	agaattatta
gacatgttag	caagagcaga	aagagagaag	aaaggcggcg	gtgtcactag	ccccaaaggcc
ctggaggagg	ccccctggcc	cccgccggaa	ggggccttcg	tgggctttgt	gctttcccg
aaggagccca	tgtgggcccga	tcttctggcc	ctggccgcgcg	ccaggggggg	ccgggtccac
cgggcccccg	agccttataa	agccctcagg	gacctgaagg	aggcgcgggg	gcttctcgcc
aaagacctga	gcgttctggc	cctgagggaa	ggccttggcc	tcccgcggcg	cgacgacccc
atgctcctcg	cctacctcct	ggacccttcc	aacaccaccc	ccgagggggg	ggcccggcg
tacggcgggg	agtggacgga	ggaggcgggg	gagcgggccg	ccctttccga	gaggctcttc
gccaacctgt	gggggaggct	tgagggggag	gagaggctcc	tttggtttta	ccgggagggtg
gagaggcccc	tttccgctgt	cctggccccc	atggaggcca	cgggggtgcg	cctggacgtg
gcctatctca	gggccttgct	cctggaggtg	gccgaggaga	tcgcccgcct	cgaggccgag
gtcttccg	tgcccgccca	ccccttcaac	ctcaactccc	gggaccagct	ggaaaagggtc
ctctttgacg	agctagggct	tcccgcctac	ggcaagacgg	agaagaccgg	caagcgctcc
accagcgccg	ccgtcctgga	ggccctccgc	gaggccacc	ccatcggtga	gaagatcctg
cagtaccggg	agctcaccaa	gctgaagagc	acctacattg	acccttgcc	ggacctcatc

caccaccagga cggggccgct ccacaccgc ttcaaccaga cggccacggc cacgggcagg
 ctaagtagct ccgatcccaa cctccagaac atccccgtcc gcaccccgct tgggcagagg
 atccgccggg ccttcatcgc cgaggagggg tggctattgg tggccctgga ctatagccag
 atagagctca ggggtgctggc ccacctctcc ggcgacgaga acctgatccg ggtcttcag
 gaggggaggc acatccacac ggagaccgcc agctggatgt tcggcgctcc cgggagggcc
 gtggaccccc tgatgcgcg ggcgcccaag accatcaact tcggggctct ctacggcatg
 tcggccccc gccctctcca gagctagcc atcccttacg aggaggccca ggcttcatt
 gagcgctact ttcagagctt ccccaagggt cgggctgga ttgagaagac cctggaggag
 ggcaggaggc ggggggtacgt ggagaccctc ttcggccgcc gccgctacgt gccagacct
 gagggccggg tgaagagcgt gcgggaggcg gccgagcgca tggccttcaa catgcccgtc
 cagggcaccg ccgccgacct catgaagctg gctatggtga agctcttccc caggctggag
 gaaatgggg ccaggatgct ccttcaggtc caccgacgagc tggtcctcga ggcccaaaa
 gagaggggc aggcctggc ccggctggc aaggaggtca tggaggggt gtatccctg
 gccgtgccc tggaggtgga ggtggggata ggggaggact ggctctccg caaggaggc
 attgatggc gcggcgagg cgggcatcat catcatcatc attaa

SEQ ID NO: 129 The amino acid sequence of the Sac7d-ΔTaq fusion protein

MITNSTVKVKFKYKGEEKEVDTSKIKKVWRVVGKMSFTYDDNGKTGRGAVSEKDA
 PKELLDMLARAEREKKGGGVTSKALEEAPWPPPEGAFVGFVLSRKEPMWADLLAL
 AAAGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLL
 DPSNTTPEGVARRYGGWEETEEAGERAAALSERLFANLWGRLEGEERLLWLYREVERP
 LSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERV
 LFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTCLKSTYIDPLPLDI
 HPRTGRLHTRFNQTATATGRLSSDPNLQNPVRTPLGQRIRRAFIAEEGWLLVALDY
 SQIELRVLAHLSDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFG
 VLYGMSAHRLSQELAIPEEAQAFIERYFQSFPKVRWIEKTLEEGRRRGYVETLFG
 RRYVPDLEARVKSREAAERMAFNMPVQGTAAADLMKMLAMVKLFPRL EEMGARM
 LQVHDELVLEAPKERA EAVARLAKEVMGVYPLAVPLEVEVGIGEDWLSAKEGIDG
 RGGGGHHHHHH

SEQ ID NO: 130 The DNA sequence encoding the PL-ΔTaq fusion protein

ATGATTACGAATTCGAAGAAAAAGAAAAAGAAAAAGCGTAAGAAACGCAAAAA
 GAAAAAGAAAGGCGGCGGTGTCACTAGTGGCGCAACCGTAAAGTTCAAGTACAA
 AGGCGAAGAAAAAGAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGG
 GCAAGATGATCTCCTTACCTACGACGAGGCGGTGGCAAGACCGGCCGTGGTG
 CGGTAAGCGAAAAAGGACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAG
 AAAAAGGGCGGCGGTGTCAACAGTCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC
 CCGCCGAAGGGGCTTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGG
 CCGATCTTCTGGCCCTGGCCGCCGAGGGGGGGCGGGTCCACCGGGCCCCCG
 AGCCTTATAAAGCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAG
 ACCTGAGCGTTCTGGCCCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCC
 CATGCTCCTCGCCTACCTCCTGGACCTTCCAACACCACCCCGAGGGGGTGGCC
 CGGCGCTACGGCGGGGAGTGGACGGAGGAGGCGGGGAGCGGGGCCGCCCTTTC
 GAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTT
 TGGCTTTACCGGAGGTGGAGAGGCCCCCTTCCGCTGTCTGGCCCATGGAGG
 CCACGGGGGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGC
 CGAGGAGATCGCCCGCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTC
 AACCTCAACTCCCGGGACAGCTGGAAGGGTCTCTTTGACGAGCTAGGGCTTC
 CCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCGTCC
 TGGAGGCCCTCCGCGAGGCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGG
 AGCTACCAAGCTGAAGAGCACCTACATTGACCCCTTGCCGACCTCATCCACC
 CAGGACGGGCCGCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAG
 GCTAAGTAGCTCCGATCCCAACCTCCAGAACATCCCGTCCGCACCCCGCTTGGG
 CAGAGGATCCGCGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTG
 GACTATAGCCAGATAGAGCTCAGGGTGCTGGCCACCTCTCCGGCGACGAGAAC
 CTGATCCGGGTCTTCCAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGG

ATGTTTCGGCGTCCCCCGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAG
ACCATCAACTTCGGGGTCTCTACGGCATGTCTGGCCCCACCGCCTCTCCCAGGAGC
TAGCCATCCCTTACGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTT
CCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGG
GGTACGTGGAGACCCTCTTCGGCCGCCCGCTACGTGCCAGACCTAGAGGCCC
GGGTGAAGAGCGTGCGGGAGGCCGCGCATGGCCTTCAACATGCCCGTCC
AGGGCACCGCCGCCACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCT
GGAGGAAATGGGGGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGA
GGCCCCAAAAGAGAGGGCGGAGGCCGTGGCCCGGTGGCCAAGGAGGTCATGG
AGGGGGTGTATCCCTGGCCGTGCCCTGGAGGTGGAGGTGGGGATAGGGGAGG
ACTGGCTCTCCGCCAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATC
ATCATCATCATTA

SEQ ID NO: 131 The amino acid sequence of PL- ΔTaq fusion protein

MITNSKKKKKKRKKRKKKKGGGVTS GATVVKFKYKGEEKEVDISKIKKVWRVVK
MISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKGGGVTS PKALEEAPWPPPEG
AFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVL
ALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFAN
LWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLE
AEVFRLAGHPFNLNSRDQLERVLFDLGLPAIGKTEKTGKRSTSAAVLEALREAHPIV
EKILQYRELTKLKSTYIDPLDLHPRTGRLHTRFNQTATATGRLSSSDPNLQNPVTRP
LGQRIRAFIAEEGWLLVALDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMF
GVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPEYEAQAFIERYFQSFPKVR
AWIEKTLEEGRRRGYVETLFGRRRYVPDLEARVKS VREAAERMAFNMPVQGTAA
LMKLAMVKLFPRL EEMGARMLLQVHDEL VLEAPKERAEAVARLAKEVMEGVYPL
AVPLEVEVGIGEDWLSAKEGIDGRGGGGHHHHHH

SEQ ID NO: 132 PRIMER L71F 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQ ID NO: 133 PRIMER L71R 5'-GCACAGCGGCTGGCTGAGGA-3'

SEQ ID NO: 134 PRIMER L18015F 15 5'-TGACGGAGGATAACGCCAGCAG-3'

SEQ ID NO: 135 PRIMER L23474R 5'-GAAAGACGA TGGGTCGCTAATACGC-3'

SEQ ID NO: 136 PRIMER L18015F 5'-TGACGGAGGATAAC GCCAGCAG-3'

SEQ ID NO: 137 PRIMER L29930R 5'-GGGGTTGGAGGTCAATGGGTTC-3'

SEQ ID NO: 138 PRIMER L3035OF 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQ ID NO: 139 PRIMER L3512IR 30 5'-CACATGGTACAGCAAGCCTGGC-3'

SEQ ID NO: 140 PRIMER L2089F 5'-CCCGTATCTGCTGGGA TACTGGC-3'

SEQ ID NO: 141 PRIMER L7112R 5'-CAGCGGTGCTGACTGAATCATGG-3'

SEQ ID NO: 142 PRIMER L3035OF 5'-CCTGCCTGCCGCTTCACGC-3'

SEQ ID NO: 143 PRIMER L40547R 5'-CCAATACCCGTTTCA TCGCGGC-3'

SEQ ID NO: 144 PRIMER H-Amelo-Y 5'-CCACCTCATCCTGG GCACC-3'

SEQ ID NO: 145 PRIMER H-Amelo-YR 5'-GCTTGAGGCCAACCATCAGAGC-3'

SEQ ID NO: 146 Human beta-globin primer 536F 5'-GGTTGGCCAATCTACTCCCAGG-3'

SEQ ID NO: 147 Human beta-globin primer 536R 5'-GCTCACTCAGTGTGGCAAAG-3'

SEQ ID NO: 148 Human beta-globin primer 1408R 5'-GATTAGCAAAAGGGCCTAGCTTGG- 3'

Figure 20

PURIFIED THERMOSTABLE PYROCOCCLUS FURIOSUS DNA POLYMERASE I

AMINO ACID SEQUENCE (SEQ ID NO: 62)

Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
50 55 60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65 70 75 80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
85 90 95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
210 215 220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225 230 235 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
245 250 255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu	275	280	285
Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn	290	295	300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr	305	310	315
Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu	325	330	335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu	340	345	350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala	355	360	365
Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser	370	375	380
Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn	385	390	395
Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr	405	410	415
His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr	420	425	430
Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly	435	440	445
Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile	450	455	460
Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu	465	470	475
Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly	485	490	495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu	500	505	510
Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu	515	520	525
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly	530	535	540
Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys	545	550	555
Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu	565	570	575

Replacement Figure

Glu	Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Val	Thr	Lys			
				580				585					590					
Lys	Arg	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Gly	Lys	Val	Ile	Thr	Arg	Gly			
				595			600					605						
Leu	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln			
	610					615					620							
Ala	Arg	Val	Leu	Glu	Thr	Ile	Leu	Lys	His	Gly	Asp	Val	Glu	Glu	Ala			
625					630					635					640			
Val	Arg	Ile	Val	Lys	Glu	Val	Ile	Gln	Lys	Leu	Ala	Asn	Tyr	Glu	Ile			
				645				650						655				
Pro	Pro	Glu	Lys	Leu	Ala	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Pro	Leu	His			
			660					665					670					
Glu	Tyr	Lys	Ala	Ile	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Lys	Leu	Ala			
		675					680					685						
Ala	Lys	Gly	Val	Lys	Ile	Lys	Pro	Gly	Met	Val	Ile	Gly	Tyr	Ile	Val			
	690					695					700							
Leu	Arg	Gly	Asp	Gly	Pro	Ile	Ser	Asn	Arg	Ala	Ile	Leu	Ala	Glu	Glu			
705					710					715					720			
Tyr	Asp	Pro	Lys	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn			
				725					730					735				
Gln	Val	Leu	Pro	Ala	Val	Leu	Arg	Ile	Leu	Glu	Gly	Phe	Gly	Tyr	Arg			
			740					745					750					
Lys	Glu	Asp	Leu	Arg	Tyr	Gln	Lys	Thr	Arg	Gln	Val	Gly	Leu	Thr	Ser			
		755					760					765						
Trp	Leu	Asn	Ile	Lys	Lys	Ser												
	770					775												

PURIFIED THERMOSTABLE PYROCOCCLUS FURIOSUS DNA POLYMERASE I

NUCLEOTIDE SEQUENCE (SEQ ID NO: 61)

ccctggtcct	gggtccacat	atatgttctt	actgccttt	atgaagaatc	ccccagtcgc	60
tctaacctgg	ggtatagtga	caaattcttc	tccaccaccg	ccaagaagg	ttatttctat	120
caactctaca	ctccccctat	tttctctctt	atgagatttt	taagtatagt	tatagagaag	180
gttttatact	ccaaactgag	ttagtagata	tgtggggagc	ataatgattt	tagatgtgga	240
ttacataact	gaagaaggaa	aacctgttat	taggctattc	aaaaaagaga	acggaaaatt	300
taagatagag	catgatagaa	cttttagacc	atacatctac	gctcttctca	gggatgattc	360
aaagattgaa	gaagttaaga	aaataacggg	ggaaaggcat	ggaaagattg	tgagaattgt	420

Replacement Figure

tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta	480
tttggacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt	540
tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct	600
aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta	660
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa	720
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag	780
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat	840
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact	900
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga	960
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag	1020
gacaataaat ctccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc	1080
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga	1140
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt	1200
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag	1260
gtcaagcaca gggaaccttg tagagtgggt cttacttagg aaagcctacg aaagaaacga	1320
agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac	1380
aggtaggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt	1440
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct	1500
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat	1560
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac	1620
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc	1680
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta	1740
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg	1800
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta	1860
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa	1920
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt ttataagag	1980
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac	2040
tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag	2100
agttttggag acaataactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga	2160

Replacement Figure

agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca	2220
gataacaaga ccattacatg agtataaggc gataggctcct cacgtagctg ttgcaaagaa	2280
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag	2340
aggcgatggc ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca	2400
caagtatgac gcagaatatt acattgagaa ccagggttctt ccagcgggtac ttaggatatt	2460
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct	2520
aacttcttgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt	2580
tctaaccctt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta	2640
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc	2700
tttgctaagt gaatagaata aacaacatca ctcaattcaa acgccttcgt tagaaatggc	2760
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct	2820
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct	2880
tcaagatttt ctaaaagaat tttaacggcc tctcgtcaa tttcgacgac gtagatcttt	2940
tttgctccaa gcagagccgc tccaatggat aacaccctg ttcccgacc caagtccgct	3000
acaatttttt ccttgatatc cctaattgat aagcaagcca aaggagagta gatgctacct	3060
ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg	3120
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt	3180
taacttttác agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta	3240
ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc	3300
ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta	3360
gacactcaaa taccagacga caatgggtgtg ctcaactcaag ccccatatgg gttgagaaaa	3420
gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntccnga	3480
aagattgaga tgttcttgg	3499